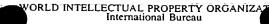# PCT

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(54) Title: *CHLAMYDIA PNEUMONIAE* GENOMIC SEQUENCE AND POLYPEPTIDES, FRAGMENTS THEREOF AND USES THEREOF, IN PARTICULAR FOR THE DIAGNOSIS, PREVENTION AND TREATMENT OF INFECTION

(57) Abstract

The subject of the invention is the genomic sequence and the nucleotide sequences encoding polypeptides of *Chlamydia pneumoniae*, such as cellular envelope polypeptides, which are secreted or specific, or which are involved in metabolism, in the replication process or in virulence, polypeptides encoded by such sequences, as well as vectors including the said sequences and cells or animals transformed with these vectors. The invention also relates to transcriptional gene products of the *Chlamydia pneumoniae* genome, such as, for example, antisense and ribozyme molecules, which can be used to control growth of the microorganism. The invention also relates to methods of detecting these nucleic acids or polypeptides and kits for diagnosing *Chlamydia pneumoniae* infection. The invention also relates to a method of selecting compounds capable of modulating bacterial infection and a method for the biosynthesis or biodegradation of molecules of interest using the said nucleotide sequences or the said polypeptides. The invention finally comprises, pharmaceutical, in particular vaccine, compositions for the prevention and/or treatment of bacterial, in particular *Chlamydia pneumoniae*, infections.

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CHLAMYDIA PNEUMONIAE GENOMIC SEQUENCE AND POLYPEPTIDES, FRAGMENTS THEREOF AND USES THEREOF, IN PARTICULAR FOR THE DIAGNOSIS, PREVENTION AND TREATMENT OF INFECTION

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10 polypeptides encoded by such sequences, as well as vectors including the said sequences and cells or animals transformed with these vectors. The invention also relates to transcriptional gene products of the *Chlamydia pneumoniae* genome, such as, for example, antisense and ribozyme molecules, which can be used to control growth of the microorganism. The invention also relates to methods of detecting these nucleic acids or polypeptides and kits for diagnosing *Chlamydia pneumoniae* infection.

15 The invention also relates to a method of selecting compounds capable of modulating bacterial infection and a method for the biosynthesis or biodegradation of molecules of interest using the said nucleotide sequences or the said polypeptides. The invention finally comprises, pharmaceutical, in particular vaccine, compositions for the prevention and/or treatment of bacterial, in particular *Chlamydia pneumoniae*, infections.

20 Comparative analysis of the sequence of the gene encoding the ribosomal 16S RNA has been widely used for the phylogenetic study of prokaryotes. This approach has made it possible to classify the Chlamydiae among the eubacteria, among which they represent a well-isolated group, with, nevertheless, a very weak link with the planctomyces. The Chlamydiae thus exhibit some unique characteristics within the eubacteria, in particular their development cycle and the structure of their

25 membranes. They have a unique two-phase cell cycle: the elementary body, a small extracellular form, attaches to the host and is phagocytosed; in the phagosome, it is converted to the replicative intracellular form, the reticulate body. The Chlamydiae are obligate intracellular bacteria which multiply in eukaryotic cells at the expense of their energy reserves and nucleotide pools; they are responsible for a wide variety of diseases in mammals and birds. The Chlamydiae are the only

30 members of the order Chlamydiales, of the family Chlamydiaceae and of the genus Chlamydia. Within the genus *Chlamydia*, four species are currently described: *Chlamydia trachomatis*, *Chlamydia psittaci*, *Chlamydia pneumoniae* and *Chlamydia pecorum*. These bacteria are grouped together and share biological and biochemical properties. Among them, only the first three infect humans, *Chlamydia pecorum* being a pathogen of ruminants.

35 The species *Chlamydia psittaci* infects many animals, in particular birds, and is transmissible to humans. It is responsible for atypical pneumonia, for hepatic and renal dysfunction, for endocarditis and for conjunctivitis.

The species *Chlamydia trachomatis* is the best characterized. Besides a murine strain, it is divided into two groups which are distinguishable by the nature of the diseases for which they are responsible: trachoma, genital attack and venereal lymphogranulomatosis. There are fifteen human serotypes of *Chlamydia trachomatis* (A, K) and LGV (L1, L2, L3). Strains A to C are mainly found in

5   eye infections, whereas strains D to K and LGV are essentially responsible for genital entry infections. It should be mentioned that the LGV strains are responsible for systemic diseases. Historically, it was in 1906 that Halberstaeder and Von Provaseck discovered, in trachoma patients, the presence of inclusions in the cytoplasm of the cells derived from conjunctival scrapings. In 1940, Rake and Jones described these same inclusions in certain cells obtained by puncturing the ganglia from a patient

10   suffering from venereal granulomatosis. Characterization of the *Chlamydia trachomatis* microorganism was only successfully carried out in 1957, after a series of isolations in cell cultures.

It was in 1983 that *Chlamydia pneumoniae* was recognized as a human pathogen (Grayston JT et al., 1986); since then, special attention has been paid to this bacterium and it is estimated (Gaydos CA et al., 1994) that 10% of pneumonias, and 5% of bronchitides and sinusites are

15   attributable to *Chlamydia pneumoniae* (Aldous MB et al., 1992). More recently, the association of this bacterium with the pathogenesis of asthmatic disease and of cardiovascular impairments is increasingly of interest.

Serological studies have made it possible to observe that *Chlamydia pneumoniae* infection is common in children between 5 and 16 years of age. Before this age, it is rare to find

20   antibodies; the increase in the number of individuals carrying antibodies is then correlated with age up to 20 years. Accordingly, 50% of adults are carriers of antibodies, it being possible for this prevalence to be as high as 75%. These figures are all the more striking since a first infection induces antibody levels of which the persistence over time is limited to 3 or at most 5 years, which suggests frequent reinfection during the entire lifespan. The annual seroconversion rate is about 8% between 8 and

25   12 years and about 6% between 12 and 16 years (Haidl et al., 1994). Before the age of 15 years, the seroprevalence of the disease is identical between both sexes. After this age, men are more frequently infected than women; this is true in all regions worldwide where such studies have been carried out.

These infections are geographically highly widespread, as shown by numerous studies carried out throughout the world (Kanamoto Y et al., 1991; Tong CY et al., 1993). Developed

30   countries of the north such as Canada, Denmark and Norway have the lowest infection rates; conversely, the highest prevalence rates are found in the less developed countries of tropical regions where the infection may occur before the age of 5 years.

Humans are the only known reservoir for *Chlamydia pneumoniae* and it is probable that the infection is caused by direct transmission, respiratory secretions probably being responsible for

35   this low-yield transmission (Aldous et al., 1992). The chain of transmission may also appear to be indirect (Kleemola M et al., 1988), suggesting that the infection is caused by an effective transmission, but also that asymptomatic carriers exist, which could explain the high prevalence of the disease.

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Other studies (Mordhorst CH et al., 1992) show that the efficiency of the transmission varies according to the individuals and list cases of infection affecting all or the majority of members of one family or of a group of families. The period of incubation is several weeks, significantly longer in this regard than that of many other respiratory pathogenic agents. Although under conditions of high

5 relative humidity the infectivity of *Chlamydia pneumoniae* in the open air decreases rapidly, süggesting a direct mode of transmission under these conditions, it is probable that the transmission occurs in some cases indirectly since the microorganism can survive for up to 30 hours in a hostile environment (Falsey et al., 1993).

Clinical manifestations due to *Chlamydia pneumoniae* are essentially respiratory

10 diseases. Pneumonia and bronchitis are the most frequent because they are clinically patent: since etiological diagnosis is evoked in this case, the infectious agent is identified. The asymptomatic diseases are probably numerous (Grayston JT et al., 1992; Grayston JT et al., 1986; Thom DH et al., 1990). The disease then progresses via bronchitis or pneumonia; fever is absent at the time of examination but is sometimes reported by the patient. The degree of seriousness of the disease is

15 variable and in hospitalized patients, it is common to observe pleural effusion; a generalized infection may also be observed and, in severe cases, anatomicopathological examination shows *Chlamydia pneumoniae* diseases.

Other syndromes such as sinusitis (Hashiguchi K et al., 1992), purulent otitis media (Ogawa H et al., 1992), or pharyngitis (Huovinen P et al., 1989) have been described, as well as

20 infections with respiratory impairments similar to asthma (Hahn DL et al., 1991). *Chlamydia pneumoniae* has also been associated with sarcoidosis, with erythema nodosum (Sundelof et al., 1993) and one case of Guillain-Barré syndrome has even been described (Haidl et al., 1992). The involvement of *Chlamydia pneumoniae* in Reiter's syndrome has also been evaluated (Braun J et al., 1994).

25 The association of *Chlamydia pneumoniae* with coronary diseases and with myocardial infarction was first suspected from the observation of the high antibody level in 71% of patients having a heart disease (Shor A et al., 1992; Kuo CC et al., 1993; Puolakkainen M et al., 1993; Thomas GN et al., 1997). Studies carried out in several countries have shown similar results in patients with atheromatous impairments (Shor A et al., 1992; Kuo CC et al., 1993; Puolakkainen M

30 et al., 1993; Grayston JT et al., 1996; Casas-Ciria J et al., 1996; Thomas GN et al., 1997; Jackson LA et al., 1997) and in patients with carotid impairments. Anatomicopathological and microbiological studies have detected *Chlamydia pneumoniae* in the vessels. The electron microscope has made it possible to visualize the bacterium (Ladany S et al., 1989), which has in fact been demonstrated by other techniques such as PCR (Campbell LA et al., 1992; Kuo CC et al., 1993; Kuo CC et al., 1988). It

35 also appears that the bacterium is more frequently found in old atheromatous lesions. Other studies carried out on young subjects from 15 to 35 years have given the opportunity to study the coronary arteries of people without atherosclerosis, this observation not being possible in older subjects (the

onset of the atheromatous disease is early). In these young subjects, the PCR studies did not find *Chlamydia pneumoniae* in subjects free of atheromatous disease, but revealed the presence of *Chlamydia pneumoniae* in two of the eleven subjects who showed early lesions and in six of the seven subjects who developed atheroma plaques. These studies therefore show that the atheroma plaque is

5 very strongly correlated with the presence of *Chlamydia pneumoniae*, but the role played by the bacterium in vascular pathology is not yet defined.

The data relating to controlled clinical studies analysing the effect of treatments in *Chlamydia pneumoniae* infections are limited in number. Unlike penicillin, ampicillin or the sulphamides, erythromycin, tetracycline or doxycycline show an antibiotic activity *in vitro* against

10 *Chlamydia pneumoniae*. However, a treatment at high doses should be continued for several weeks in order to avoid a recurrence of the infection. Accordingly, the use of two new macrolides, clarithromycin and azithromycin, whose diffusion, bioavailability and half-life allow shorter and better tolerated cures, is nowadays preferred. In the absence of definitive proof based on the results of clinical studies, an effective, without recurrences, and well-tolerated treatment of *Chlamydia*

15 *prieumoniae* infections therefore remains desirable.

An even more important need up until now relates to a specific and sensitive diagnosis, which can be carried out conveniently and rapidly, allowing early screening for the infection. Methods based on *Chlamydia pneumoniae* culture are slow and require a considerable know-how because of the difficulty involved in the collection, preservation and storage of the strain under appropriate

20 conditions. Methods based on antigen detection (EIA, DFA) or on nucleic acid amplification (PCR) provide tests which are more suitable for laboratory practice. A reliable, sensitive and convenient test, which allows distinction between serogroups and a fortiori between *Chlamydia pneumoniae* species is therefore highly desirable.

This is all the more important since the symptoms of *Chlamydia pneumoniae* infection

25 appear slowly, since all the pathologies associated with these infections have not yet been identified, and since, as has been mentioned above, an association is suspected between these infections and serious chronic infections, asthma or atherosclerosis.

No vaccine is yet available against *Chlamydia pneumoniae*: this is due to the labile nature of the antigens specific to the strain, which has so far prevented their specific identification.

30 Although the number of studies and of animal models developed is high, the antigens used have not induced sufficient protective immunity to lead to the development of human vaccines. In the case of *Chlamydia pneumoniae*, the role of the immune defense in the physiology and pathology of the disease should probably be understood in order to develop satisfactory vaccines.

More detailed information relating to the biology of these strains, their interactions with

35 their hosts, the associated phenomena of infectivity and those of escaping the immune defenses of the host in particular, and finally their involvement in the development of the these associated pathologies, will allow a better understanding of these mechanisms. In the light of the preceding text which shows

in particular the limitations of the means of controlling *Chlamydia pneumoniae* infection, it is therefore at present essential, on the one hand, to develop molecular tools, in particular from a better genetic knowledge of *Chlamydia pneumoniae*, but also to develop new preventive and therapeutic treatments, new diagnostic methods and new vaccine strategies which are specific, effective and tolerated. This is precisely the object of the present invention.

The subject of the present invention is the nucleotide sequence having the sequence SEQ ID No. 1 of the *Chlamydia pneumoniae* genome. However, the invention is not limited to SEQ ID No. 1, but encompasses genomes and nucleotides encoding polypeptides of strain variants, polymorphisms, allelic variants, and mutants.

Thus, the subject of the present invention encompasses nucleotide sequences characterized in that they are chosen from:

a) the nucleotide sequence of SEQ ID No. 1, a nucleotide sequence exhibiting at least 99.9% identity with the sequence SEQ ID No. 1, the nucleotide sequence of the genomic DNA contained within ATCC Deposit No. ___, the nucleotide sequence of a clone insert within ATCC Deposit No. __;

b) a nucleotide sequence homologous to the sequence SEQ ID No. 1;

c) a polynucleotide sequence that hybridizes to the nucleotide sequence of a) under conditions of high or intermediate stringency as described below:

(i) By way of example and not limitation, procedures using conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 h to overnight at 65EC in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 μg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65EC, the preferred hybridization temperature, in prehybridization mixture containing 100 μg/ml denatured salmon sperm DNA and 5-20 X 10^6 cpm of ^{32}P-labeled probe. Alternatively, the hybridization step can be performed at 65EC in the presence of SSC buffer, 1 x SSC corresponding to 0.15M NaCl and 0.05 M Na citrate. Subsequently, filter washes can be done at 37EC for 1 h in a solution containing 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA, followed by a wash in 0.1X SSC at 50EC for 45 min. Alternatively, filter washes can be performed in a solution containing 2 x SSC and 0.1% SDS, or 0.5 x SSC and 0.1% SDS, or 0.1 x SSC and 0.1% SDS at 68EC for 15 minute intervals. Following the wash steps, the hybridized probes are detectable by autoradiography. Other conditions of high stringency which may be used are well known in the art and as cited in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety.

(ii) By way of example and not limitation, procedures using conditions of intermediate stringency are as follows: Filters containing DNA are prehybridized, and then hybridized at a

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temperature of 60EC in the presence of a 5 x SSC buffer and labeled probe. Subsequently, filters washes are performed in a solution containing 2x SSC at 50EC and the hybridized probes are detectable by autoradiography. Other conditions of intermediate stringency which may be used are well known in the art and as cited in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual,

5   Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety.

    d) a nucleotide sequence complementary to the sequence SEQ ID No. 1 or complementary to a nucleotide sequence as defined in a), b) or c) and a nucleotide

10   sequence of their corresponding RNA;

    e) a nucleotide sequence of a representative fragment of the sequence SEQ ID No. 1, or of a representative fragment of the nucleotide sequence as defined in a), b), c) or d);

    f) a nucleotide sequence comprising a sequence as defined in a), b), c), d) or e);

    g) a nucleotide sequence capable of being obtained from a nucleotide sequence as defined

15   in a), b), c), d), e) or f); and

    h) a modified nucleotide sequence of a nucleotide sequence as defined in a), b), c), d), e), f) or g).

    Nucleotide sequence, polynucleotide or nucleic acid are understood to mean, according to the present invention, either a double-stranded DNA, a single-stranded DNA or products of

20   transcription of the said DNAs.

    It should be understood that the present invention does not relate to the genomic nucleotide sequences of *Chlamydia pneumoniae* taken in their natural environment, that is to say in the natural state. They are sequences which may have been isolated, purified or partially purified, by separation methods such as, for example, ion-exchange chromatography, molecular size exclusion

25   chromatography or affinity chromatography, or alternatively fractionation techniques based on solubility in various solvents, or by genetic engineering methods such as amplification, cloning or subcloning, it being possible for the sequences of the invention to be carried by vectors.

    The nucleotide sequence SEQ ID No. 1 was obtained by sequencing the *Chlamydia pneumoniae* genome by the method of directed sequencing after fluorescent automated sequencing of

30   the inserts of clones and assembling of these sequences of nucleotide fragments (inserts) by means of softwares (cf. Examples). In spite of the high precision of the sequence SEQ ID No. 1, it is possible that it does not perfectly, 100% represent the nucleotide sequence of the *Chlamydia pneumoniae* genome and that a few rare sequencing errors or uncertainties still remain in the sequence SEQ ID No. 1. In the present invention, the presence of an uncertainty for an amino acid is designated

35   by "Xaa" and that for a nucleotide is designated by "N" in the sequence listing below. These few rare errors or uncertainties could be easily detected and corrected by persons skilled in the art using the entire chromosome and/or its representative fragments according to the invention and standard

amplification, cloning and sequencing methods, it being possible for the sequences obtained to be easily compared, in particular by means of a computer software and using computer-readable media for recording the sequences according to the invention as described, for example, below. After correcting these possible rare errors or uncertainties, the corrected nucleotide sequence obtained would

5   still exhibit at least 99.9% identity with the sequence SEQ ID No. 1. Such rare sequencing uncertainties are not present within the DNA contained within ATCC Deposit No. __ or ___, and whatever rare sequence uncertainties that exist within SEQ ID No. 1 can routinely be corrected utilizing the DNA of the ATCC deposits.

Homologous nucleotide sequence for the purposes of the present invention is understood

10 to mean a nucleotide sequence having a percentage identity with the bases of the nucleotide sequence SEQ ID No. 1 of at least 80%, preferably 90% and 95%, this percentage being purely statistical and it being possible for the differences between the two nucleotide sequences to be distributed randomly and over their entire length. The said homologous sequences exhibiting a percentage identity with the bases of the nucleotide sequence SEQ ID No. 1 of at least 80%, preferably 90% and 95%, may

15 comprise, for example, the sequences corresponding to the genomic sequence or to the sequences of its representative fragments of a bacterium belonging to the Chlamydia family, including the species *Chlamydia trachomatis*, *Chlamydia psittaci* and *Chlamydia pecorum* mentioned above, as well as the sequences corresponding to the genomic sequence or to the sequences of its representative fragments of a bacterium belonging to the variants of the species *Chlamydia pneumoniae*. In the present

20 invention, the terms family and genus are mutually interchangeable, the terms variant, serotype, strain and subspecies are also mutually interchangeable. These homologous sequences may thus correspond to variations linked to mutations within the same species or between species and may correspond in particular to truncations, substitutions, deletions and/or additions of at least one nucleotide. The said homologous sequences may also correspond to variations linked to the degeneracy of the genetic code

25 or to a bias in the genetic code which is specific to the family, to the species or to the variant and which are likely to be present in *Chlamydia*.

Protein and/or nucleic acid sequence homologies may be evaluated using any of the variety of sequence comparison algorithms and programs known in the art. Such algorithms and programs include, but are by no means limited to, TBLASTN, BLASTP, FASTA, TFASTA, and

30 CLUSTALW (Pearson and Lipman, 1988, *Proc. Natl. Acad. Sci. USA 85(8)*:2444-2448; Altschul *et al.*, 1990, *J. Mol. Biol. 215(3)*:403-410; Thompson *et al.*, 1994, *Nucleic Acids Res. 22(2)*:4673-4680; Higgins *et al.*, 1996, *Methods Enzymol. 266*:383-402; Altschul *et al.*, 1990, *J. Mol. Biol. 215(3)*:403-410; Altschul *et al.*, 1993, *Nature Genetics 3*:266-272).

In a particularly preferred embodiment, protein and nucleic acid sequence homologies are

35 evaluated using the Basic Local Alignment Search Tool ("BLAST") which is well known in the art (see, *e.g.*, Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. USA 87*:2267-2268; Altschul *et al.*, 1990, *J. Mol. Biol. 215*:403-410; Altschul *et al.*, 1993, *Nature Genetics 3*:266-272; Altschul *et al.*, 1997,

Nuc. Acids Res. *25*:3389-3402). In particular, five specific BLAST programs are used to perform the following task:

> (1)BLASTP and BLAST3 compare an amino acid query sequence against a protein sequence database;

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> (2)BLASTN compares a nucleotide query sequence against a nucleotide sequence database;

> (3)BLASTX compares the six-frame conceptual translation products of a query nucleotide sequence (both strands) against a protein sequence database;

> (4)TBLASTN compares a query protein sequence against a nucleotide sequence database

10

> translated in all six reading frames (both strands); and

> (5)TBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence

15 and a test sequence which is preferably obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are preferably identified (*i.e.*, aligned) by means of a scoring matrix, many of which are known in the art. Preferably, the scoring matrix used is the BLOSUM62 matrix (Gonnet *et al.*, 1992, *Science 256*:1443-1445; Henikoff and Henikoff, 1993, *Proteins 17*:49-61). Less preferably, the PAM or PAM250 matrices may also be used (see, *e.g.*, Schwartz and Dayhoff, eds.,

20 1978, *Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure*, Washington: National Biomedical Research Foundation)

The BLAST programs evaluate the statistical significance of all high-scoring segment pairs identified, and preferably selects those segments which satisfy a user-specified threshold of significance, such as a user-specified percent homology. Preferably, the statistical significance of a

25 high-scoring segment pair is evaluated using the statistical significance formula of Karlin (see, *e.g.*, Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. USA 87*:2267-2268).

Nucleotide sequence complementary to a sequence of the invention is understood to mean any DNA whose nucleotides are complementary to those of the sequence of the invention, and whose orientation is reversed (antiparallel sequence).

30 The present invention further comprises fragments of the sequences of a) through f), above. Representative fragments of the sequences according to the invention will be understood to mean any nucleotide fragment having at least 8 successive nucleotides, preferably at least 12 successive nucleotides, and still more preferably at least 15 or at least 20 successive nucleotides of the sequence from which it is derived. It is understood that such fragments refer only to portions of SEQ

35 ID No. 1 that are not currently listed in a publicly available database.

Among these representative fragments, those capable of hybridizing under stringent conditions with a nucleotide sequence according to the invention are preferred. Hybridization under

stringent conditions means that the temperature and ionic strength conditions are chosen such that they allow hybridization to be maintained between two complementary DNA fragments.

By way of illustration, high stringency conditions for the hybridization step for the purposes of defining the nucleotide fragments described above, are advantageously the following.

5   The hybridization is carried out at a preferred temperature of 65EC in the presence of SSC buffer, 1 × SSC corresponding to 0.15 M NaCl and 0.05 M Na citrate. The washing steps may be, for example, the following:

2 × SSC, 0.1% SDS at room temperature followed by three washes with 1 × SSC, 0.1% SDS;
0.5 × SSC, 0.1% SDS; 0.1 × SSC, 0.1% SDS at 68EC for 15 minutes.

10   Intermediate stringency conditions, using, for example, a temperature of 60EC in the presence of a 5 × SSC buffer, or of low stringency, for example a temperature of 50EC in the presence of a 5 × SSC buffer, respectively require a lower overall complementarity for the hybridization between the two sequences.

The stringent hybridization conditions described above for a polynucleotide of about
15   300 bases in size will be adapted by persons skilled in the art for larger- or smaller-sized oligonucleotides, according to the teaching of Sambrook et al., 1989.

Among the representative fragments according to the invention, those which can be used as primer or probe in methods which make it possible to obtain homologous sequences or their representative fragments according to the invention, or to reconstitute a genomic fragment found to be
20   incomplete in the sequence SEQ ID No. 1 or carrying an error or an uncertainty, are also preferred, these methods, such as the polymerase chain reaction (PCR), cloning and sequencing of nucleic acid being well known to persons skilled in the art. These homologous nucleotide sequences corresponding to mutations or to inter- or intra-species variations, as well as the complete genomic sequence or one of its representative fragments capable of being reconstituted, of course form part of
25   the invention.

Among the said representative fragments, those which can be used as primer or probe in methods allowing diagnosis of the presence of *Chlamydia pneumoniae* or one of its associated microorganisms as defined below are also preferred.

The representative fragments capable of modulating, regulating, inhibiting or inducing
30   the expression of a gene of *Chlamydia pneumoniae* or one of its associated microorganisms, and/or capable of modulating the replication cycle of *Chlamydia pneumoniae* or one of its associated microorganisms in the host cell and/or organism, are also preferred. Replication cycle is intended to designate invasion, multiplication, intracellular localization, in particular retention in the vacuole and inhibition of the process of fusion to the lysosome, and propagation of *Chlamydia pneumoniae* or one
35   of its associated microorganisms from host cells to host cells.

Among the said representative fragments, those corresponding to nucleotide sequences corresponding to open reading frames, called ORF sequences (ORF for open reading frame), and

encoding polypeptides, such as for example, but   without being limited thereto, the ORF sequences which will be later described, are finally preferred.

The representative fragments according to the invention may be obtained, for example, by specific amplification, such as PCR, or after digestion, with appropriate restriction enzymes, of 5 nucleotide sequences according to the invention; these methods are in particular described in the manual by Sambrook et al., 1989.   The said representative fragments may also be obtained by chemical synthesis when they are not too large in size and according to methods well known to persons skilled in the art. For example, such fragments can be obtained by isolating fragments of the genomic DNA of ATCC Deposit No. ___ or a clone insert present at this ATCC Deposit No. __.

10   The representative fragments according to the invention may be used, for example, as primer, to reconstitute some of the said representative fragments, in particular those in which a portion of the sequence is likely to be missing or imperfect, by methods well known to persons skilled in the art such as amplification, cloning or sequencing techniques.

Modified nucleotide sequence will be understood to mean any nucleotide sequence 15 obtained by mutagenesis according to techniques well known to persons skilled in the art, and exhibiting modifications in relation to the normal sequences, for example mutations in the regulatory and/or promoter sequences for the expression of a polypeptide, in particular leading to a modification of the level of expression of the said polypeptide or to a modulation of the replicative cycle.

Modified nucleotide sequence will also be understood to mean any nucleotide sequence 20 encoding a modified polypeptide as defined below.

The subject of the present invention also includes *Chlamydia pneumoniae* nucleotide sequences characterized in that they are chosen from a nucleotide sequence of an open reading frame (ORF), that is, the ORF2 to ORF1297 sequences.

The ORF2 to ORF1297 nucleotide sequences are defined in Tables 1 and 2, *infra*, by 25 their position on the sequence SEQ ID No. 1. For example, the ORF2 sequence is defined by the nucleotide sequence between the nucleotides at position 42 and 794 on the sequence SEQ ID No. 1, ends included. ORF2 to ORF1297 have been identified via homology analyses as well as via analyses of potential ORF start sites, as discussed in the examples below. It is to be understood that each identified ORF of the invention comprises a nucleotide sequence that spans the contiguous nucleotide 30 sequence from the ORF stop codon immediately 3' to the stop codon of the preceding ORF and through the 5' codon to the next stop codon of SEQ ID No.:1 in-frame to the ORF nucleotide sequence. Table 2, *infra*, lists the beginning, end and potential start site of each of ORFs 1-1297. In one embodiment, the ORF comprises the contiguous nucleotide sequence spanning from the potential ORF start site downstream (that is, 3') to the ORF stop codon (or the ORF codon immediately adjacent 35 to and upstream of the ORF stop codon). ORF2 to ORF1297 encode the polypeptides of SEQ ID No. 2 to SEQ ID No. 1291 and of SEQ ID No. 6844 to SEQ ID No. 6849, respectively.

Upon introduction of minor frameshifts, certain individual ORFs can comprise larger

"combined" ORFs. A list of such putative "combined" ORFs is shown in Table 3, below.
For example, a combined ORF can comprise ORF 25, ORF 26 and ORF 27, including intervening in-
frame, nucleotide sequences. The order of ORFs (5' to 3'), within each "combined" ORF is as listed.
It is to be understood that when ORF2 to ORF1297 are referred to herein, such reference is also meant
5   to include "combined" ORFs. Polypeptide sequences encoded by such "combined" ORFs are also part
of the present invention.

Table 3

ORF 25, ORF 26, ORF 27;

10   ORF 28, ORF 29, ORF 30;

ORF 31, ORF 32;

ORF 33, ORF 35;

ORF 466, ORF 467;

ORF 468, ORF 469;

15   ORF 477, ORF 476, ORF 474;

ORF 480, ORF 482;

ORF 483, ORF 485, ORF 486, ORF 500;

ORF 503, ORF 504, ORF 505;

ORF 506, ORF 507;

20   ORF 1211, ORF 647;

ORF 1286, ORF 1039;

ORF 691, ORF 690;

ORF 105, ORF 106;

ORF 170, ORF 171;ORF 394, ORF 393;

25   ORF 453, ORF 452, ORF 451;

ORF 526, ORF 525;

ORF 757, ORF 756, ORF 755;

ORF 856, ORF 855;

ORF 958, ORF 957;

30   ORF 915, ORF 914, ORF 913;

ORF 543, ORF 544;

ORF 1266, ORF 380;

ORF 745, ORF 744;

ORF 777, ORF 776;

35   ORF 343, ORF 1297, and representative fragments.

Table 1 also depicts the results of homology searches that compared the sequences of the

12

polypeptides encoded by each of the ORFs to sequences present in public published databases. It is understood that those polypeptides listed in Table 1 as exhibiting greater than about 95% identity to a polypeptide present in a publicly disclosed database are not considered part of the present invention; likewise in this embodiment, those nucleotide sequences encoding such polypeptides are

5 not considered part of the invention. In another embodiment, it is understood that those polypeptides listed in Table 1 as exhibiting greater than about 99% identity to a polypeptide present in a publicly disclosed database are not considered part of the invention; likewise, in this embodiment, those nucleotide sequences encoding such polypeptides are not considered part of the invention.

The invention also relates to the nucleotide sequences characterized in that they comprise

10 a nucleotide sequence chosen from:

a)   an ORF2 to ORF1297, a "combined" ORF nucleotide sequence, the nucleotide sequence of the genomic DNA contained within ATCC Deposit No. _____ or the nucleotide sequence of a clone insert in ATCC Deposit No. _____ according to the invention;

b)   a homologous nucleotide sequence exhibiting at least 80% identity across an entire ORF2 to

15 ORF1297 nucleotide sequence according to the invention or as defined in a);

c)   a polynucleotide sequence that hybridizes to ORF2 to ORF1297 under conditions of high or intermediate stringency as described below:

(i) By way of example and not limitation, procedures using conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 h to overnight at 65EC in

20 buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 µg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65EC, the preferred hybridization temperature, in prehybridization mixture containing 100 µg/ml denatured salmon sperm DNA and 5-20 X 10^6 cpm of ^{32}P-labeled probe. Alternatively, the hybridization step can be performed at 65EC in the presence of SSC buffer, 1 x SSC corresponding to 0.15M NaCl and

25 0.05 M Na citrate. Subsequently, filter washes can be done at 37EC for 1 h in a solution containing 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA, followed by a wash in 0.1X SSC at 50EC for 45 min. Alternatively, filter washes can be performed in a solution containing 2 x SSC and 0.1% SDS, or 0.5 x SSC and 0.1% SDS, or 0.1 x SSC and 0.1% SDS at 68EC for 15 minute intervals. Following the wash steps, the hybridized probes are detectable by autoradiography. Other conditions of high

30 stringency which may be used are well known in the art and as cited in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual,   Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety. Preferably, such sequences encode a homolog of a polypeptide encoded by one of ORF2 to ORF1297. In one

35 embodiment, such sequences encode a *Chlamydia pneumoniae* polypeptide.

(ii)   By way of example and not limitation, procedures using conditions of intermediate

stringency are as follows: Filters containing DNA are prehybridized, and then hybridized at a temperature of 60EC in the presence of a 5 x SSC buffer and labeled probe. Subsequently, filters washes are performed in a solution containing 2x SSC at 50EC and the hybridized probes are detectable by autoradiography. Other conditions of intermediate stringency which may be used are

5   well known in the art and as cited in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety. Preferably, such sequences encode a homolog of a polypeptide encoded by one of ORF2 to ORF1297. In one embodiment, such sequences encode a *Chlamydia*

10   *pneumoniae* polypeptide.

d)   complementary or RNA nucleotide sequence corresponding to an ORF2 to ORF1297 sequence according to the invention or as defined in a), b) or c);

e)   a nucleotide sequence of a representative fragment of an ORF2 to ORF1297 sequence according to the invention or of a sequence as defined in a), b), c) or d);

15   f)   a nucleotide sequence capable of being obtained from an ORF2 to ORF1297 sequence according to the invention or as defined in a), b), c), d) or e); and

g)   a modified nucleotide sequence of an ORF2 to ORF1297 sequence according to the invention or as defined in a), b), c), d), e) or f);

As regards the homology with the ORF2 to ORF1297 nucleotide sequences, the

20   homologous sequences exhibiting a percentage identity with the bases of one of the ORF2 to ORF1297 nucleotide sequences of at least 80%, preferably 90% and 95%, are preferred. Such homologous sequences are identified routinely via, for example, the algorithms described above and in the examples below. The said homologous sequences correspond to the homologous sequences as defined above and may comprise, for example, the sequences corresponding to the ORF sequences of

25   a bacterium belonging to the Chlamydia family, including the species *Chlamydia trachomatis*, *Chlamydia psittaci* and *Chlamydia pecorum* mentioned above, as well as the sequences corresponding to the ORF sequences of a bacterium belonging to the variants of the species *Chlamydia pneumoniae*. These homologous sequences may likewise correspond to variations linked to mutations within the same species or between species and may correspond in particular to truncations, substitutions,

30   deletions and/or additions of at least one nucleotide. The said homologous sequences may also correspond to variations linked to the degeneracy of the genetic code or to a bias in the genetic code which is specific to the family, to the species or to the variant and which are likely to be present in *Chlamydia*.

The invention comprises polypeptides encoded by a nucleotide sequence according to the

35   invention, preferably by a representative fragment of the sequence SEQ ID No. 1 and corresponding to an ORF sequence, in particular the *Chlamydia pneumoniae* polypeptides, characterized in that they are chosen from the sequences SEQ ID No. 2 to SEQ ID No. 1291 or SEQ ID No. 6844 to SEQ ID No.

6849 and representative fragments thereof. However, the invention is not limited to polypeptides encoded by ORFs in SEQ ID No. 1 and its corresponding ORF sequences, but encompasses polypeptides of strain variants, polymorphisms, allelic variants, and mutants.

Thus, the invention also comprises the polypeptides characterized in that they comprise a

5   polypeptide chosen from:

a)   a polypeptide encoded by a polynucleotide sequence in SEQ ID No. 1 (*e.g.*, any polypeptide encoded by a polynucleotide sequence corresponding to ORF2 to ORF1297 and/or representative fragments thereof) according to the invention;

b)   a polypeptide homologous to a polypeptide according to the invention, or as defined in a);

10 c)   a polypeptide encoded by a polynucleotide sequence that hybridizes to SEQ ID No. 1 or ORF2 to ORF1297 under high or intermediate stringency as described below:

(i) By way of example and not limitation, procedures using conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 h to overnight at 65EC in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll,

15 0.02% BSA, and 500 µg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65EC, the preferred hybridization temperature, in prehybridization mixture containing 100 µg/ml denatured salmon sperm DNA and 5-20 X 10^6 cpm of ^{32}P-labeled probe. Alternatively, the hybridization step can be performed at 65EC in the presence of SSC buffer, 1 x SSC corresponding to 0.15M NaCl and 0.05 M Na citrate. Subsequently, filter washes can be done at 37EC for 1 h in a solution containing

20 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA, followed by a wash in 0.1X SSC at 50EC for 45 min. Alternatively, filter washes can be performed in a solution containing 2 x SSC and 0.1% SDS, or 0.5 x SSC and 0.1% SDS, or 0.1 x SSC and 0.1% SDS at 68EC for 15 minute intervals. Following the wash steps, the hybridized probes are detectable by autoradiography. Other conditions of high stringency which may be used are well known in the art and as cited in Sambrook et al., 1989,

25 Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety. Preferably such polypeptide represents a homolog of a polypeptide encoded by ORF2 to ORF1297. Preferably, such sequences encode a homolog of a polypeptide encoded by one of ORF2 to ORF1297. In one embodiment, such

30 sequences encode a *Chlamydia pneumoniae* polypeptide.

(ii) By way of example and not limitation, procedures using conditions of intermediate stringency are as follows: Filters containing DNA are prehybridized, and then hybridized at a temperature of 60EC in the presence of a 5 x SSC buffer and labeled probe. Subsequently, filters washes are performed in a solution containing 2x SSC at 50EC and the hybridized probes are

35 detectable by autoradiography. Other conditions of intermediate stringency which may be used are well known in the art and as cited in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual,

Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current

Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are

incorporated herein in their entirety. Preferably, such sequences encode a homolog of a polypeptide

encoded by one of ORF2 to ORF1297. In one embodiment, such sequences encode a *Chlamydia*

5 *pneumoniae* polypeptide.

d)   a fragment of at least 5 amino acids of a polypeptide according to the invention, or as defined in

a), b) or c);

e)   a biologically active fragment of a polypeptide according to the invention, or as defined in a), b),

c) or d); and

10 f)   a modified polypeptide of a polypeptide according to the invention, as defined in a), b), c),d) or

e).

In the present description, the terms polypeptide, peptide and protein are interchangeable.

It should be understood that the invention does not relate to the polypeptides in natural

form, that is to say that they are not taken in their natural environment but that they may have been

15 isolated or obtained by purification from natural sources, or alternatively obtained by genetic

recombination, or else by chemical synthesis and that they may, in this case, comprise nonnatural

amino acids, as will be described below.

Homologous polypeptide will be understood to designate the polypeptides exhibiting, in

relation to the natural polypeptide, certain modifications such as in particular a deletion, addition or

20 substitution of at least one amino acid, a truncation, an extension, a chimeric fusion, and/or a mutation,

or polypeptides exhibiting post-translational modifications. Among the homologous polypeptides,

those whose amino acid sequence exhibits at least 80%, preferably 90%, homology or identity with the

amino acid sequences of the polypeptides according to the invention are preferred. In the case of a

substitution, one or more consecutive or nonconsecutive amino acids are replaced by "equivalent"

25 amino acids. The expression "equivalent" amino acid is intended here to designate any amino acid

capable of being substituted for one of the amino acids in the basic structure without, however,

essentially modifying the biological activities of the corresponding peptides and as will be defined

later.

Protein and/or nucleic acid sequence homologies may be evaluated using any of the

30 variety of sequence comparison algorithms and programs known in the art. Such algorithms and

programs include, but are by no means limited to, TBLASTN, BLASTP, FASTA, TFASTA, and

CLUSTALW (Pearson and Lipman, 1988, *Proc. Natl. Acad. Sci. USA 85(8)*:2444-2448; Altschul *et

al.*, 1990, *J. Mol. Biol. 215(3)*:403-410; Thompson *et al.*, 1994, *Nucleic Acids Res. 22(2)*:4673-4680;

Higgins *et al.*, 1996, *Methods Enzymol. 266*:383-402; Altschul *et al.*, 1990, *J. Mol. Biol. 215(3)*:403-

35 410; Altschul *et al.*, 1993, *Nature Genetics 3*:266-272).

In a particularly preferred embodiment, protein and nucleic acid sequence homologies are

evaluated using the Basic Local Alignment Search Tool ("BLAST") which is well know in the art (see,

e.g., Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. USA* 87:2267-2268; Altschul *et al.*, 1990, *J. Mol. Biol. 215*:403-410; Altschul *et al.*, 1993, *Nature Genetics 3*:266-272; Altschul *et al.*, 1997, *Nuc. Acids Res. 25*:3389-3402). In particular, five specific BLAST programs are used to perform the following task:

5   (1)BLASTP and BLAST3 compare an amino acid query sequence against a protein sequence database;

(2)BLASTN compares a nucleotide query sequence against a nucleotide sequence database;

(3)BLASTX compares the six-frame conceptual translation products of a query

10   nucleotide sequence (both strands) against a protein sequence database;

(4)TBLASTN compares a query protein sequence against a nucleotide sequence database translated in all six reading frames (both strands); and

(5)TBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

15   The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is preferably obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are preferably identified (*i.e.*, aligned) by means of a scoring matrix, many of which are known in the art. Preferably, the scoring matrix used is the BLOSUM62 matrix (Gonnet

20   *et al.*, 1992, *Science 256*:1443-1445; Henikoff and Henikoff, 1993, *Proteins 17*:49-61). Less preferably, the PAM or PAM250 matrices may also be used (see, *e.g.*, Schwartz and Dayhoff, eds., 1978, *Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure*, Washington: National Biomedical Research Foundation)

The BLAST programs evaluate the statistical significance of all high-scoring segment

25   pairs identified, and preferably selects those segments which satisfy a user-specified threshold of significance, such as a user-specified percent homology. Preferably, the statistical significance of a high-scoring segment pair is evaluated using the statistical significance formula of Karlin (see, *e.g.*, Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. USA 87*:2267-2268).

Equivalent amino acids may be determined either based on their structural homology

30   with the amino acids for which they are substituted, or on results of comparative tests of biological activity between the various polypeptides which may be carried out.

By way of example, there may be mentioned the possibilities of substitutions which may be carried out without resulting in a substantial modification of the biological activity of the corresponding modified polypeptides; the replacements, for example, of leucine with valine or

35   isoleucine, of aspartic acid with glutamic acid, of glutamine with asparagine, of arginine with lysine, and the like, the reverse substitutions naturally being feasible under the same conditions.

The homologous polypeptides also correspond to the polypeptides encoded by the

homologous nucleotide sequences as defined above and thus comprise in the present definition the mutated polypeptides or polypeptides corresponding to inter- or intra-species variations which may exist in *Chlamydia*, and which correspond in particular to truncations, substitutions, deletions and/or additions of at least one amino acid residue.

5   Biologically active fragment of a polypeptide according to the invention will be understood to designate in particular a polypeptide fragment, as defined below, exhibiting at least one of the characteristics of the polypeptides according to the invention, in particular in that it is:

- capable of eliciting an immune response directed against *Chlamydia pneumoniae*; and/or
- capable of being recognized by an antibody specific for a polypeptide according to the invention;
10   and/or
- capable of binding to a polypeptide or to a nucleotide sequence of *Chlamydia pneumoniae*; and/or
- capable of modulating, regulating, inducing or inhibiting the expression of a gene of *Chlamydia pneumoniae* or one of its associated microorganisms, and/or capable of modulating the replication cycle of *Chlamydia pneumoniae* or one of its associated microorganisms in the
15   host cell and/or organism; and/or
- capable of generally exerting an even partial physiological activity, such as for example a structural activity (cellular envelope, ribosome), an enzymatic (metabolic) activity, a transport activity, an activity in the secretion or in the virulence.

A polypeptide fragment according to the invention is understood to designate a
20 polypeptide comprising a minimum of 5 amino acids, preferably 10 amino acids or preferably 15 amino acids. It is to be understood that such fragments refer only to portions of polypeptides encoded by ORF2 to ORF1297 that are not currently listed in a publicly available database.

The polypeptide fragments according to the invention may correspond to isolated or purified fragments which are naturally present in *Chlamydia pneumoniae* or which are secreted by
25 *Chlamydia pneumoniae*, or may correspond to fragments capable of being obtained by cleaving the said polypeptide with a proteolytic enzyme, such as trypsin or chymotrypsin or collagenase, or with a chemical reagent, such as cyanogen bromide (CNBr) or alternatively by placing the said polypeptide in a highly acidic environment, for example at pH 2.5. Such polypeptide fragments may be equally well prepared by chemical synthesis, using hosts transformed with an expression vector according to
30 the invention containing a nucleic acid allowing the expression of the said fragments, placed under the control of appropriate elements for regulation and/or expression.

"Modified polypeptide" of a polypeptide according to the invention is understood to designate a polypeptide obtained by genetic recombination or by chemical synthesis as will be described below, exhibiting at least one modification in relation to the normal sequence. These
35 modifications may in particular affect amino acids responsible for a specificity or for the efficiency of the activity, or responsible for the structural conformation, for the charge or for the hydrophobicity, and for the capacity for multimerization and for membrane insertion of the polypeptide according to

18

the invention. It is thus possible to create polypeptides with an equivalent, an increased or a reduced activity, and with an equivalent, a narrower or a broader specificity. Among the modified polypeptides, there may be mentioned the polypeptides in which up to 5 amino acids may be modified, truncated at the N- or C-terminal end, or alternatively deleted, or else added.

5   As is indicated, the modifications of the polypeptide may have in particular the objective:

-   of making it capable of modulating, regulating, inhibiting or inducing the expression of a gene of *Chlamydia*, in particular of *Chlamydia pneumoniae* and its variants, or one of its associated microorganisms, and/or capable of modulating the replication cycle of *Chlamydia*, in particular of *Chlamydia pneumoniae* and its variants, or one of its associated microorganisms,

10   in the host cell and/or organism,

-   of allowing its use in methods of biosynthesis or of biodegradation, or its incorporation into vaccine compositions,

-   of modifying its bioavailability as a compound for therapeutic use.

          The said modified polypeptides may also be used on any cell or microorganism for which

15 the said modified polypeptides will be capable of modulating, regulating, inhibiting or inducing gene expression, or of modulating the growth or the replication cycle of the said cell or of the said microorganism. The methods allowing demonstration of the said modulations on eukaryotic or prokaryotic cells are well known to persons skilled in the art. The said cells or microorganisms will be chosen, in particular, from tumour cells or infectious microorganisms and the said modified

20 polypeptides may be used for the prevention or treatment of pathologies linked to the presence of the said cells or of the said microorganisms. It is also clearly understood that the nucleotide sequences encoding the said modified polypeptides may be used for the said modulations, for example by the intermediacy of vectors according to the invention and which are described below, so as to prevent or to treat the said pathologies.

25   The above modified polypeptides may be obtained using combinatory chemistry, in which it is possible to systematically vary portions of the polypeptide before testing them on models, cell cultures or microorganisms for example, so as to select the compounds which are the most active or which exhibit the desired properties.

          Chemical synthesis also has the advantage of being able to use:

30   - nonnatural amino acids, or

          - nonpeptide bonds.

          Accordingly, in order to extend the life of the polypeptides according to the invention, it may be advantageous to use nonnatural amino acids, for example in the D form, or alternatively amino acid analogues, in particular sulphur-containing forms for example.

35   Finally, the structure of the polypeptides according to the invention, its homologous or modified forms, as well as the corresponding fragments may be integrated into chemical structures of the polypeptide type and the like. Accordingly, it may be advantageous to provide at the N- and C-

terminal ends compounds which are not recognized by proteases.

Also forming part of the invention are the nucleotide sequences encoding a polypeptide according to the invention. Described below are ORF nucleotide sequences encoding polypeptides exhibiting particularly preferable characteristics. For each group of preferred ORFS described below,

5   it is to be understood that in addition to the individual ORFs listed, in instances wherein such ORFS are present as part of "combined" ORFs, the "combined" ORFs are also to be included within the preferred group.

More particularly, the subject of the invention is nucleotide sequences, characterized in that they encode a polypeptide of the cellular envelope, preferably of the outer cellular envelope of

10   *Chlamydia pneumoniae* or one of its representative fragments, such as for example the predominant proteins of the outer membrane, the adhesion proteins or the proteins entering into the composition of the Chlamydia wall. Among these sequences, the sequences comprising a nucleotide sequence chosen from the following sequences are most preferred:

ORF15; ORF25; ORF26; ORF27; ORF28; ORF29; ORF30; ORF31; ORF32; ORF33; ORF35;

15   ORF68; ORF124; ORF275; ORF291; ORF294; ORF327; ORF342; ORF364; ORF374; ORF380; ORF414; ORF439; ORF466; ORF467; ORF468; ORF469; ORF470; ORF472; ORF474; ORF476; ORF477; ORF478; ORF479; ORF480; ORF482; ORF485; ORF500; ORF501; ORF503; ORF504; ORF505; ORF506; ORF520; ORF578; ORF580; ORF581; ORF595; ORF596; ORF597; ORF737; ORF830; ORF834; ORF836; ORF893; ORF917; ORF932; ORF976; ORF1035; ORF1045; ORF1090

20   and one of their representative fragments.

The structure of the cytoplasmic membranes and of the wall of bacteria is dependent on the associated proteins. The structure of the cytoplasmic membrane makes it impermeable to water, to water-soluble substances and to small-sized molecules (ions, small inorganic molecules, peptides or proteins). To enter into or to interfere with a cell or a bacterium, a ligand must establish a special

25   relationship with a protein anchored in the cytoplasmic membrane (the receptor). These proteins which are anchored on the membrane play an important role in metabolism since they control the exchanges in the bacterium. These exchanges apply to molecules of interest for the bacterium (small molecules such as sugars and small peptides) as well as undesirable molecules for the bacterium such as antibiotics or heavy metals.

30   The double lipid layer structure of the membrane requires the proteins which are inserted therein to have hydrophobic domains of about twenty amino acids forming an alpha helix. Predominantly hydrophobic and potentially transmembrane regions may be predicted from the primary sequence of the proteins, itself deduced from the nucleotide sequence. The presence of one or more putative transmembrane domains raises the possibility for a protein to be associated with the

35   cytoplasmic membrane and to be able to play an important metabolic role therein or alternatively for the protein thus exposed to be able to exhibit potentially protective epitopes.

If the proteins inserted into the membrane exhibit several transmembrane domains

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capable of interacting with one another via electrostatic bonds, it then becomes possible for these proteins to form pores which go across the membrane which becomes permeable for a number of substances. It should be noted that proteins which do not have transmembrane domains may also be anchored by the intermediacy of fatty acids in the cytoplasmic membrane, it being possible for the

5   breaking of the bond between the protein and its anchor in some cases to be responsible for the release of the peptide outside the bacterium.

Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* transmembrane polypeptide or one of its representative fragments, having between 1 and 3 transmembrane domains and in that they comprise a

10 nucleotide sequence chosen from the following sequences:

ORF2; ORF3; ORF6; ORF9; ORF10; ORF11; ORF13; ORF14; ORF16; ORF18; ORF19; ORF20; ORF21; ORF22; ORF25; ORF27; ORF28; ORF29; ORF30; ORF31; ORF32; ORF33; ORF34; ORF35; ORF37; ORF39; ORF41; ORF42; ORF44; ORF45; ORF46; ORF47; ORF48; ORF49; ORF50; ORF53; ORF54; ORF56; ORF57; ORF59; ORF60; ORF61; ORF62; ORF63; ORF64;

15 ORF65; ORF66; ORF69;; ORF72; ORF73; ORF74; ORF76; ORF77; ORF78; ORF79; ORF80; ORF82; ORF84; ORF85; ORF86; ORF88; ORF89; ORF90; ORF91; ORF92; ORF93; ORF95; ORF96; ORF98; ORF99; ORF100; ORF101; ORF102; ORF103; ORF104; ORF105; ORF106; ORF107; ORF108; ORF114; ORF117; ORF118; ORF122; ORF123; ORF124; ORF125; ORF129; ORF130; ORF131; ORF132; ORF133; ORF134; ORF135; ORF137; ORF138; ORF139; ORF140;

20 ORF141; ORF142; ORF143; ORF145; ORF146; ORF147; ORF150; ORF151; ORF152; ORF156; ORF157; ORF158; ORF159; ORF160; ORF161; ORF162; ORF164; ORF166; ORF167; ORF170; ORF173; ORF175; ORF176; ORF178; ORF179; ORF180; ORF182; ORF183; ORF184; ORF185; ORF186; ORF187; ORF188; ORF189; ORF190; ORF191; ORF192; ORF194; ORF195; ORF196; ORF197; ORF198; ORF199; ORF200; ORF201; ORF202; ORF205; ORF207; ORF208; ORF209;

25 ORF210; ORF212; ORF215; ORF219; ORF220; ORF224; ORF226; ORF227; ORF228; ORF231; ORF232; ORF233; ORF234; ORF235; ORF236; ORF238; ORF239; ORF240; ORF241; ORF242; ORF244; ORF247; ORF251; ORF252; ORF253; ORF255; ORF256; ORF257; ORF258; ORF260; ORF262; ORF263; ORF266; ORF267; ORF268; ORF269; ORF270; ORF273; ORF274; ORF276; ORF278; ORF279; ORF280; ORF281; ORF282; ORF283; ORF284; ORF286; ORF287; ORF289;

30 ORF290; ORF291; ORF293; ORF294; ORF297; ORF304; ORF305; ORF307; ORF308; ORF309; ORF310; ORF311; ORF313; ORF314; ORF315; ORF316; ORF318; ORF319; ORF320; ORF321; ORF322; ORF323; ORF324; ORF325; ORF326; ORF331; ORF332; ORF336; ORF338; ORF339; ORF341; ORF344; ORF345; ORF346; ORF350; ORF352; ORF353; ORF356; ORF357; ORF358; ORF359; ORF360; ORF362; ORF365; ORF366; ORF367; ORF370; ORF372; ORF373; ORF376;

35 ORF377; ORF378; ORF379; ORF381; ORF382; ORF383; ORF384; ORF385; ORF386; ORF387; ORF390; ORF392; ORF393; ORF394; ORF396; ORF398; ORF399; ORF400; ORF404; ORF408; ORF410; ORF411; ORF413; ORF416; ORF417; ORF418; ORF420; ORF422; ORF424; ORF427;

21

ORF428; ORF429; ORF430; ORF431; ORF433;   ORF434; ORF437; ORF440; ORF441; ORF442;
ORF443; ORF444; ORF445; ORF447; ORF450; ORF451; ORF452; ORF455; ORF456; ORF459;
ORF460; ORF461; ORF462; ORF463; ORF464; ORF465; ORF467; ORF469; ORF471; ORF474;
ORF475; ORF476; ORF477; ORF479; ORF482; ORF483; ORF484; ORF485; ORF486; ORF487;

5 ORF488; ORF491; ORF493; ORF494; ORF497; ORF498; ORF499; ORF503; ORF508; ORF509;
ORF510; ORF512; ORF514; ORF515; ORF516; ORF517; ORF518; ORF520; ORF521; ORF523;
ORF525; ORF527; ORF528; ORF529; ORF530; ORF531; ORF533; ORF534; ORF535; ORF536;
ORF537; ORF540; ORF541; ORF543; ORF544; ORF545; ORF546; ORF548; ORF549; ORF551;
ORF553; ORF554; ORF555; ORF556; ORF557; ORF558; ORF559; ORF560; ORF562; ORF563;

10 ORF564; ORF565; ORF566; ORF569; ORF571; ORF573; ORF576; ORF577; ORF581; ORF583;
ORF584; ORF585; ORF586; ORF588; ORF591; ORF592; ORF594; ORF595; ORF596; ORF597;
ORF599; ORF600; ORF603; ORF605; ORF608; ORF614; ORF615; ORF620; ORF621; ORF622;
ORF623; ORF624; ORF625; ORF629; ORF630; ORF631; ORF633; ORF634; ORF637; ORF642;
ORF644; ORF645; ORF647; ORF648; ORF652; ORF654; ORF655; ORF657; ORF658; ORF659;

15 ORF660; ORF661; ORF664; ORF665; ORF666; ORF667; ORF670; ORF671; ORF672; ORF673;
ORF674; ORF676; ORF679; ORF681; ORF684; ORF687; ORF688; ORF689; ORF690; ORF693;
ORF694; ORF695; ORF696; ORF697; ORF698; ORF699; ORF700; ORF701; ORF703; ORF705;
ORF706; ORF707; ORF708; ORF710; ORF712; ORF715; ORF716; ORF717; ORF718; ORF719;
ORF721; ORF722; ORF723; ORF725; ORF726; ORF727; ORF728; ORF729; ORF730; ORF731;

20 ORF733; ORF736; ORF737; ORF738; ORF740; ORF741; ORF742; ORF743; ORF747; ORF748;
ORF750; ORF752; ORF754; ORF755; ORF756; ORF757; ORF759; ORF760; ORF761; ORF762;
ORF763; ORF764; ORF765; ORF766; ORF767; ORF768; ORF772; ORF774; ORF775; ORF777;
ORF781; ORF783; ORF788; ORF791; ORF792; ORF793; ORF794; ORF795; ORF796; ORF797;
ORF798; ORF799; ORF802; ORF803; ORF806; ORF807; ORF808; ORF809; ORF810; ORF811;

25 ORF813; ORF814; ORF815; ORF816; ORF817; ORF819; ORF820; ORF821; ORF823; ORF824;
ORF827; ORF829; ORF830; ORF831; ORF833; ORF834; ORF835; ORF837; ORF844; ORF845;
ORF846; ORF847; ORF848; ORF849; ORF850; ORF851; ORF852; ORF854; ORF855; ORF856;
ORF857; ORF859; ORF860; ORF862; ORF865; ORF866; ORF868; ORF869; ORF870; ORF871;
ORF872; ORF874; ORF877; ORF878; ORF879; ORF880; ORF881; ORF882; ORF884; ORF885;

30 ORF888; ORF889; ORF890; ORF891; ORF892; ORF894; ORF895; ORF896; ORF897; ORF899;
ORF900; ORF902; ORF903; ORF904; ORF905; ORF909; ORF910; ORF912; ORF913; ORF914;
ORF915; ORF917; ORF918; ORF919; ORF921; ORF923; ORF924; ORF926; ORF927; ORF928;
ORF929; ORF930; ORF931; ORF937; ORF938; ORF939; ORF941; ORF943; ORF948; ORF951;
ORF952; ORF953; ORF958; ORF960; ORF963; ORF964; ORF965; ORF968; ORF970; ORF974;

35 ORF975; ORF977; ORF979; ORF980; ORF981; ORF983; ORF984; ORF985; ORF987; ORF989;
ORF992; ORF993; ORF997; ORF998; ORF999; ORF1001; ORF1002; ORF1004; ORF1005;
ORF1009; ORF1013; ORF1014; ORF1015; ORF1016; ORF1019; ORF1021; ORF1023; ORF1024;

ORF1029; ORF1031; ORF1033; ORF1034; ORF1039; ORF1041; ORF1042; ORF1045; ORF1047; ORF1049; ORF1051; ORF1052; ORF1053; ORF1054; ORF1056; ORF1059; ORF1061; ORF1062; ORF1063; ORF1064; ORF1065; ORF1067; ORF1075; ORF1077; ORF1078; ORF1079; ORF1080; ORF1081; ORF1089; ORF1095; ORF1097; ORF1098; ORF1099; ORF1101; ORF1102;

5 ORF1103; ORF1106; ORF1107; ORF1108; ORF1109; ORF1110; ORF1113; ORF1116; ORF1118; ORF1119; ORF1121; ORF1123; ORF1124; ORF1126; ORF1128; ORF1130; ORF1131; ORF1133; ORF1134; ORF1136; ORF1137 and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* transmembrane polypeptide or one of its

10 representative fragments, having between 4 and 6 transmembrane domains and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF5; ORF7; ORF8; ORF15; ORF36; ORF38; ORF51; ORF55; ORF58; ORF67; ORF70; ORF81; ORF97; ORF110; ORF111; ORF115; ORF119; ORF126; ORF128; ORF148; ORF155; ORF163; ORF165; ORF168; ORF169; ORF171; ORF172; ORF174; ORF177; ORF181; ORF193; ORF203;

15 ORF213; ORF214; ORF216; ORF217; ORF221; ORF222; ORF225; ORF229; ORF243; ORF246; ORF248; ORF254; ORF261; ORF285; ORF288; ORF292; ORF296; ORF298; ORF299; ORF301; ORF303; ORF317; ORF328; ORF329; ORF351; ORF354; ORF355; ORF364; ORF371; ORF374; ORF375; ORF391; ORF395; ORF401; ORF403; ORF405; ORF409; ORF414; ORF419; ORF421; ORF423; ORF425; ORF438; ORF448; ORF453; ORF458; ORF466; ORF468; ORF470; ORF480;

20 ORF489; ORF490; ORF496; ORF501; ORF504; ORF505; ORF506; ORF511; ORF513; ORF519; ORF526; ORF532; ORF538; ORF539; ORF547; ORF550; ORF561; ORF568; ORF570; ORF574; ORF578; ORF579; ORF580; ORF582; ORF589; ORF593; ORF598; ORF601; ORF604; ORF610; ORF613; ORF617; ORF626; ORF632; ORF635; ORF638; ORF640; ORF641; ORF646; ORF649; ORF650; ORF651; ORF686; ORF711; ORF724; ORF732; ORF734; ORF744; ORF745; ORF749;

25 ORF751; ORF769; ORF770; ORF771; ORF773; ORF776; ORF779; ORF780; ORF785; ORF787; ORF789; ORF801; ORF805; ORF812; ORF822; ORF825; ORF826; ORF839; ORF841; ORF843; ORF853; ORF861; ORF875; ORF876; ORF886; ORF893; ORF898; ORF906; ORF907; ORF908; ORF920; ORF922; ORF925; ORF933; ORF935; ORF936; ORF944; ORF946; ORF947; ORF954; ORF959; ORF961; ORF966; ORF967; ORF972; ORF978; ORF995; ORF996; ORF1000; ORF1003;

30 ORF1010; ORF1011; ORF1012; ORF1017; ORF1020; ORF1030; ORF1036; ORF1038; ORF1043; ORF1046; ORF1048; ORF1050; ORF1058; ORF1071; ORF1073; ORF1084; ORF1085; ORF1086; ORF1087; ORF1091; ORF1092; ORF1094; ORF1096; ORF1100; ORF1104; ORF1111; ORF1112; ORF1114; ORF1117; ORF1122; ORF1125 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the

35 invention, characterized in that they encode a *Chlamydia pneumoniae* transmembrane polypeptide or one of its representative fragments, having at least 7 transmembrane domains and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF17; ORF52; ORF68; ORF83; ORF87; ORF109; ORF112; ORF113; ORF120; ORF121;

ORF127; ORF153; ORF204; ORF211; ORF218; ORF223; ORF275; ORF277; ORF295; ORF300;

ORF302; ORF306; ORF327; ORF335; ORF342; ORF343; ORF347; ORF349; ORF361; ORF363;

ORF369; ORF380; ORF388; ORF389; ORF397; ORF415; ORF432; ORF439; ORF446; ORF449;

5   ORF472; ORF478; ORF500; ORF522; ORF524; ORF567; ORF575; ORF602; ORF606; ORF609;

ORF636; ORF639; ORF643; ORF653; ORF668; ORF692; ORF702; ORF704; ORF713; ORF720;

ORF778; ORF784; ORF800; ORF836; ORF838; ORF842; ORF864; ORF867; ORF883; ORF901;

ORF916; ORF932; ORF934; ORF940; ORF942; ORF950; ORF956; ORF971; ORF973; ORF976;

ORF988; ORF994; ORF1018; ORF1028; ORF1035; ORF1037; ORF1044; ORF1055; ORF1057;

10   ORF1068; ORF1069; ORF1070; ORF1072; ORF1082; ORF1088; ORF1105; ORF1132; ORF1135

and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention,
characterized in that they encode a *Chlamydia pneumoniae* surface exposed polypeptide (*e.g.*, an outer
membrane protein) or one of its representative fragments, said nucleotide sequences comprising a

15   nucleotide sequence chosen from the following sequences:

ORF 15, ORF 25, ORF 26, ORF 27, ORF 28, ORF 29, ORF 30, ORF 31, ORF 32, ORF 33, ORF 35,

ORF 36, ORF 1257, ORF 280, ORF 291, ORF 314, ORF 354, ORF 380, ORF 1266, ORF 466, ORF

467, ORF 468, ORF 469, ORF 470, ORF 472, ORF 474, ORF 476, ORF 477, ORF 478, ORF 479,

ORF 480, ORF 482, ORF 483, ORF 485, ORF 486, ORF 500, ORF 501, ORF 503, ORF 504, ORF

20   505, ORF 506, ORF 507, ORF 1268, ORF 1269, ORF 543, ORF 544, ORF 578, ORF 579, ORF 580,

ORF 581, ORF 595, ORF 596, ORF 597, ORF 1271, ORF 633, ORF 637, ORF 699, ORF 706, ORF

737, ORF 744, ORF 1273, ORF 751, ORF 775, ORF 776, ORF 777, ORF 793, ORF 815, ORF 830,

ORF 1221, ORF 849, ORF 851, ORF 852, ORF 874, ORF 891, ORF 922, ORF 940, ORF 1231, ORF

1281, ORF 1035, ORF 1079, ORF 1087, ORF 1108, and one of their representative fragments.

25   Preferably, the invention relates to the nucleotide sequences according to the invention,
characterized in that they encode a *Chlamydia pneumoniae* lipoprotein or one of its representative
fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following
sequences:

ORF 3, ORF 10, ORF 11, ORF 16, ORF 1254, ORF 1255, ORF 38, ORF 1256, ORF 62, ORF 85,

30   ORF 1258, ORF 115, ORF 1151, ORF 151, ORF 1259, ORF 173, ORF 1261, ORF 186, ORF 194,

ORF 205, ORF 214, ORF 216, ORF 217, ORF 238, ORF 1177, ORF 280, ORF 291, ORF 317, ORF

327, ORF 354, ORF 364, ORF 367, ORF 414, ORF 432, ORF 1192, ORF 460, ORF 1267, ORF 1268,

ORF 520, ORF 536, ORF 1270, ORF 576, ORF 597, ORF 603, ORF 609, ORF 637, ORF 1272, ORF

652, ORF 1213, ORF 699, ORF 705, ORF 706, ORF 708, ORF 711, ORF 727, ORF 1274, ORF 800,

35   ORF 814, ORF 825, ORF 829, ORF 830, ORF 831, ORF 844, ORF 849, ORF 1275, ORF 1276, ORF

1277, ORF 872, ORF 878, ORF 880, ORF 891, ORF 892, ORF 1278, ORF 1279, ORF 1280, ORF

941, ORF 942, ORF 1282, ORF 1283, ORF 952, ORF 988, ORF 998, ORF 1009, ORF 1285, ORF

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1235, ORF 1028, ORF 1056, ORF 1070, ORF 1287, ORF 1087, ORF 1288, ORF 1289, ORF 1098, ORF 1246, ORF 1291, ORF 1108, ORF 1109, ORF 1112, ORF 1133, and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention,
5   characterized in that they encode a *Chlamydia pneumoniae* polypeptide involved in lipopolysaccharide (LPS) biosynthesis, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences: ORF 316, ORF 564, ORF 610, ORF 647, ORF 1211, ORF 688, ORF 924, and one of their representative fragments.

Preferably the invention relates to additional LPS-related nucleotide sequences according
10 to the invention, characterized in that they encode:

(a) a *Chlamydia pneumoniae* KDO (3-deoxy-D-manno-octulosonic acid)-related polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences: ORF 177, ORF 1156, ORF 245, ORF 767, and one of their representative fragments;

15   (b) a *Chlamydia pneumoniae* phosphomannomutase-related polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences: ORF 74, and one of its representative fragments;

(c) a *Chlamydia pneumoniae* phosphoglucomutase-related polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the
20 following sequences: ORF 1286, ORF 1039, and one of their representative fragments; and

(d) a *Chlamydia pneumoniae* lipid A component-related polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences: ORF 689, ORF 690, ORF 691, ORF 1037, and one of their representative fragments.

25   Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide containing RGD (Arg-Gly-Asp) attachment sites or one of its representative fragments.

(a) RGD-containing proteins that are outer membrane proteins, are more likely to play a
30   role in cell attachment. ORFs that encoded a protein containing an RGD sequence and also were classified as outer membrane proteins are ORF 468 and its representative fragments.

(b) An RGD-encoding ORF that showed homology to cds1, cds2, and copN type III
35   virulence loci in *Chlamydia psittaci* (Hsia, R. et al. (1997), Type III secretion genes identity a putative virulence locus of Chlamydia. Molecular Microbiology 25:351-359) is ORF 350, and its representative fragments.

(c) The outer membrane of Chlamydia is made of cysteine-rich proteins that form a network of both intra and inter molecular disulfide links. This contributes to the integrity of the membrane since Chlamydia lacks the peptidoglycan layer that other

5   gram-negative bacteria have. Cysteine-rich proteins that have the RGD sequence are also considered to be potential vaccine candidates. Cysteine-rich proteins were defined as proteins that had more than 3.0% cysteine in their primary amino acid sequence, above the mean genomic ORF cysteine content. The corresponding ORFs are: ORF 1290, ORF 1294, ORF 1296, and one of their representative fragments.

10

(d) The outer membrane of Chlamydia may also contain small proteins that have cysteines in their N– and C-terminus that may contribute to the network formed by disulfide linkages. These proteins may be anchored in the outer membrane via their N-terminus and may have their C-terminus exposed, which then can interact with the

15   host cells. Alternatively, these proteins may be anchored in the outer membrane via both N-and C-terminus and may have regions in the middle that may be exposed which can in turn interact with the host cells. ORFs encoding polypeptides that contain cysteines in their first 30 amino acids and also contain an RGD sequence are: ORF 105, ORF 106, ORF 114, ORF 170, ORF 171, ORF 1264, ORF 268, ORF

20   1265, ORF 350, ORF 393, ORF 394, ORF 451, ORF 452, ORF 453, ORF 473, ORF 499, ORF 515, ORF 519, ORF 525, ORF 526, ORF 538, ORF 611, ORF 645, ORF 686, ORF 700, ORF 746, ORF 755, ORF 756, ORF 757, ORF 789, ORF 814, ORF 855, ORF 856, ORF 878, ORF 957, ORF 958, ORF 989, ORF 1290, and one of their representative fragments.

25

(e) RGD-containing ORFs homologous to RGD-containing ORFs from *Chlamydia trachomatis* are:

ORF 114, ORF 468, ORF 755, ORF 756, ORF 757, ORF 855, ORF 856, ORF 905, ORF 913, ORF 914, ORF 915, and one of their representative fragments.

30

Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* Type III or other, non-type III secreted polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences:

35   ORF 25, ORF 28, ORF 29, ORF 33, ORF 308, ORF 309, ORF 343, ORF 344, ORF 345, ORF 367, ORF 414, ORF 415, ORF 480, ORF 550, ORF 579, ORF 580, ORF 581, ORF 597, ORF 699, ORF 744, ORF 751, ORF 776, ORF 866, ORF 874, ORF 883, ORF 884, ORF 888, ORF 891, ORF 1293,

and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* cell wall anchored surface polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence

5 chosen from the following sequences: ORF 267, ORF 271, ORF 419, ORF 590, ORF 932, ORF 1292, ORF 1295, and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode *Chlamydia pneumoniae* polypeptides not found in *Chlamydia trachomatis* (Blastp. P>e^{-10}), said nucleotide sequences comprising a nucleotide sequence chosen from

10 the following sequences: ORF 7, ORF 8, ORF 9, ORF 16, ORF 17, ORF 18, ORF 19, ORF 20, ORF 21, ORF 22, ORF 1254, ORF 23, ORF 1255, ORF 24, ORF 1139, ORF 1140, ORF 46, ORF 47, ORF 51, ORF 60, ORF 1256, ORF 61, ORF 62, ORF 63, ORF 64, ORF 1257, ORF 65, ORF 66, ORF 67, ORF 68, ORF 1143, ORF 1145, ORF 83, ORF 84, ORF 1146, ORF 85, ORF 86, ORF 87, ORF 1258, ORF 116, ORF 117, ORF 125, ORF 1148, ORF 143, ORF 1150, ORF 1151, ORF 144, ORF 145, ORF

15 147, ORF 148, ORF 149, ORF 150, ORF 152, ORF 1259, ORF 162, ORF 166, ORF 1154, ORF 167, ORF 1261, ORF 1156, ORF 1157, ORF 178, ORF 179, ORF 1158, ORF 182, ORF 183, ORF 184, ORF 185, ORF 1159, ORF 186, ORF 1160, ORF 187, ORF 188, ORF 189, ORF 190, ORF 1161, ORF 1162, ORF 191, ORF 192, ORF 194, ORF 195, ORF 1163, ORF 196, ORF 201, ORF 202, ORF 209, ORF 212, ORF 221, ORF 224, ORF 1167, ORF 226, ORF 227, ORF 228, ORF 229, ORF 230, ORF

20 231, ORF 232, ORF 1169, ORF 1170, ORF 1171, ORF 234, ORF 235, ORF 236, ORF 1172, ORF 243, ORF 251, ORF 252, ORF 1176, ORF 253, ORF 255, ORF 254, ORF 256, ORF 1177, ORF 1178, ORF 262, ORF 263, ORF 1264, ORF 278, ORF 279, ORF 1180, ORF 280, ORF 290, ORF 291, ORF 292, ORF 296, ORF 1181, ORF 297, ORF 298, ORF 300, ORF 1265, ORF 322, ORF 324, ORF 325, ORF 370, ORF 1186, ORF 371, ORF 372, ORF 1187, ORF 373, ORF 378, ORF 1266, ORF 382, ORF

25 383, ORF 384, ORF 385, ORF 386, ORF 1188, ORF 1189, ORF 391, ORF 392, ORF 398, ORF 400, ORF 403, ORF 1191, ORF 423, ORF 435, ORF 445, ORF 450, ORF 1193, ORF 456, ORF 460, ORF 461, ORF 465, ORF 1196, ORF 471, ORF 473, ORF 475, ORF 481, ORF 484, ORF 487, ORF 488, ORF 489, ORF 490, ORF 491, ORF 492, ORF 493, ORF 494, ORF 495, ORF 496, ORF 497, ORF 498, ORF 499, ORF 502, ORF 1267, ORF 1268, ORF 508, ORF 510, ORF 509, ORF 512, ORF 515,

30 ORF 519, ORF 1197, ORF 521, ORF 1198, ORF 522, ORF 524, ORF 528, ORF 534, ORF 537, ORF 1269, ORF 1270, ORF 548, ORF 551, ORF 557, ORF 1201, ORF 1203, ORF 562, ORF 566, ORF 593, ORF 595, ORF 600, ORF 1271, ORF 604, ORF 611, ORF 612, ORF 614, ORF 616, ORF 625, ORF 627, ORF 628, ORF 629, ORF 631, ORF 641, ORF 1272, ORF 648, ORF 1212, ORF 663, ORF 685, ORF 707, ORF 714, ORF 715, ORF 716, ORF 717, ORF 722, ORF 746, ORF 1273, ORF 761,

35 ORF 764, ORF 770, ORF 1217, ORF 783, ORF 1274, ORF 803, ORF 815, ORF 1220, ORF 835, ORF 1221, ORF 844, ORF 845, ORF 846, ORF 847, ORF 848, ORF 849, ORF 850, ORF 851, ORF 1275, ORF 852, ORF 862, ORF 1276, ORF 1277, ORF 873, ORF 1223, ORF 892, ORF 919, ORF 1225,

ORF 1278, ORF 926, ORF 1228, ORF 1229, ORF 1230, ORF 1279, ORF 1281, ORF 1282, ORF 1283, ORF 948, ORF 950, ORF 949, ORF 951, ORF 980, ORF 982, ORF 1233, ORF 999, ORF 1000, ORF 1001, ORF 1002, ORF 1008, ORF 1285, ORF 1235, ORF 1016, ORF 1019, ORF 1027, ORF 1036, ORF 1241, ORF 1048, ORF 1049, ORF 1050, ORF 1053, ORF 1054, ORF 1064, ORF 1076, ORF 1091, ORF 1288, ORF 1093, ORF 1289, ORF 1101, ORF 1103, ORF 1245, ORF 1246, ORF 1247, ORF 1290, ORF 1291, ORF 1115, ORF 1116, ORF 1118, ORF 1120, ORF 1249, ORF 1121, ORF 1250, ORF 1126, ORF 1251, ORF 1127, ORF 1128, ORF 1130, ORF 1129, ORF 1131, ORF 1136, ORF 1253, ORF 1292, ORF 1294, ORF 1295, ORF 1296, and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the intermediate metabolism, in particular in the metabolism of sugars and/or of cofactors, such as for example triose phosphate isomerase or pyruvate kinase, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF2; ORF55; ORF56; ORF69; ORF75; ORF80; ORF100; ORF110; ORF114; ORF120; ORF121; ORF157; ORF160; ORF161; ORF172; ORF180; ORF181; ORF198; ORF200; ORF225; ORF248; ORF249; ORF276; ORF277; ORF318; ORF319; ORF320; ORF323; ORF331; ORF347; ORF375; ORF376; ORF381; ORF393; ORF394; ORF395; ORF396; ORF409; ORF446; ORF447; ORF448; ORF449; ORF513; ORF516; ORF571; ORF647; ORF662; ORF697; ORF718; ORF793; ORF794; ORF808; ORF809; ORF838; ORF839; ORF840; ORF853; ORF854; ORF918; ORF923; ORF929; ORF931; ORF938; ORF939; ORF958; ORF959; ORF960; ORF966; ORF995; ORF1021; ORF1040; ORF1041; ORF1042; ORF1085; ORF1100; ORF1102; ORF1117; ORF1118; ORF1119; ORF1120; ORF1135 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the intermediate metabolism of nucleotides or nucleic acids, such as for example CTP synthetase or GMP synthetase, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF77; ORF78; ORF138; ORF189; ORF190; ORF233; ORF246; ORF338; ORF412; ORF421; ORF438; ORF607; ORF648; ORF657; ORF740; ORF783; ORF967; ORF989; ORF990; ORF992; ORF1011; ORF1058; ORF1059; ORF1073; ORF1074 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of nucleic acids, such as for example DNA polymerases or DNA topoisomerases, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF14; ORF59; ORF70; ORF71; ORF97; ORF113; ORF137; ORF141; ORF169; ORF285; ORF287;

ORF288; ORF313; ORF326; ORF358; ORF411; ORF443; ORF548; ORF569; ORF601; ORF651; ORF654; ORF658; ORF659; ORF664; ORF665; ORF694; ORF698; ORF704; ORF760; ORF762; ORF763; ORF786; ORF787; ORF788; ORF801; ORF802; ORF812; ORF819; ORF822; ORF870; ORF897; ORF898; ORF902; ORF908; ORF916; ORF954; ORF955; ORF961; ORF983; ORF996;
5 ORF1007; ORF1012; ORF1013; ORF1014; ORF1015; ORF1038; ORF1137 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of amino acids or polypeptides, such as
10 for example serine hydroxymethyl transferase or the proteins which load amino acids onto transfer RNAs, and in that they comprise a nucleotide sequence chosen from the following sequences:
ORF99; ORF111; ORF127; ORF134; ORF140; ORF174; ORF175; ORF176; ORF353; ORF377; ORF404; ORF523; ORF539; ORF559; ORF561; ORF586; ORF598; ORF609; ORF636; ORF687; ORF700; ORF701; ORF759; ORF790; ORF857; ORF861; ORF904; ORF936; ORF952; ORF962;
15 ORF963; ORF964; ORF965; ORF991; ORF1003; ORF1004; ORF1005; ORF1018; ORF1067; ORF1110; ORF1111; ORF1112; ORF1114; ORF1121; ORF1122; ORF1123; ORF1124; ORF1125 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its
20 representative fragments which is involved in the metabolism of polypeptides, such as for example protein kinases or proteases, and in that they comprise a nucleotide sequence chosen from the following sequences:
ORF4; ORF44; ORF45; ORF48; ORF54; ORF112; ORF130; ORF155; ORF163; ORF212; ORF257; ORF307; ORF343; ORF405; ORF416; ORF458; ORF540; ORF541; ORF542; ORF543; ORF544;
25 ORF560; ORF594; ORF652; ORF699; ORF723; ORF747; ORF817; ORF827; ORF871; ORF909; ORF910; ORF911; ORF912; ORF1023; ORF1051; ORF1052; ORF1081 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its
30 representative fragments which is involved in the metabolism of fatty acids, such as for example succinyl-CoA-synthesizing proteins or phosphatidylserine synthetase, and in that they comprise a nucleotide sequence chosen from the following sequences:
ORF76; ORF284; ORF308; ORF309; ORF310; ORF311; ORF312; ORF425; ORF433; ORF565; ORF688; ORF690; ORF691; ORF767; ORF797; ORF894; ORF895; ORF994; ORF1020; ORF1030;
35 ORF1033; ORF1034; ORF1046; ORF1047; ORF1057 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its

representative fragments which is involved in the synthesis of the wall, such as for example KDO transferase, and the proteins responsible for the attachment of certain sugars onto the exposed proteins, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF49; ORF50; ORF177; ORF178; ORF245; ORF610; ORF972; ORF974; ORF978; ORF1037 and

5   one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the transcription, translation and/or maturation process, such as for example initiation factors, RNA polymerases or certain chaperone proteins, and in that

10 they comprise a nucleotide sequence chosen from the following sequences:

ORF90; ORF92; ORF131; ORF151; ORF199; ORF333; ORF334; ORF336; ORF379; ORF589; ORF590; ORF619; ORF630; ORF649; ORF739; ORF741; ORF806; ORF821; ORF843; ORF968; ORF971; ORF1061 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the

15 invention, characterized in that they encode a *Chlamydia pneumoniae* ribosomal polypeptide or one of its representative fragments, such as for example the ribosomal proteins L21, L27 and S10, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF93; ORF94; ORF95; ORF136; ORF259; ORF332; ORF348; ORF583; ORF584; ORF588; ORF591; ORF592; ORF663; ORF666; ORF667; ORF669; ORF670; ORF671; ORF672; ORF673;

20 ORF674; ORF675; ORF676; ORF677; ORF678; ORF679; ORF680; ORF681; ORF683; ORF684; ORF738; ORF781; ORF1008; ORF1024; ORF1025; ORF1066 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* transport polypeptide or one of

25 its representative fragments, such as for example the proteins for transporting amino acids, sugars and certain oligopeptides, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF40; ORF41; ORF52; ORF105; ORF106; ORF107; ORF109; ORF133; ORF210; ORF211; ORF214; ORF215; ORF216; ORF217; ORF218; ORF219; ORF220; ORF223; ORF242; ORF260;

30 ORF293; ORF299; ORF366; ORF369; ORF575; ORF602; ORF638; ORF639; ORF640; ORF643; ORF653; ORF702; ORF703; ORF724; ORF732; ORF855; ORF856; ORF901; ORF906; ORF933; ORF942; ORF1043; ORF1086; ORF1105 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its

35 representative fragments which is involved in the virulence process, such as for example the proteins analogous to the *Escherichia coli* vacB protein, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF546; ORF550; ORF778; ORF779; ORF886   and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the secretory system and/or which is secreted, such as

5   for example proteins homologous to proteins in the secretory system of certain bacteria such as the Salmonellae or the Yersiniae, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF751; ORF874; ORF875; ORF876; ORF883; ORF884; ORF885 and one of their representative fragments.

10   Preferably, the invention also relates to a nucleotide sequence according to the invention, characterized in that they encode a polypeptide specific to *Chlamydia pneumoniae* or one of its representative fragments (with a Blast E value of >10^{-5}), and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF7; ORF8; ORF17; ORF18; ORF19; ORF20; ORF22; ORF23; ORF24; ORF51; ORF60; ORF63;

15 ORF65; ORF66; ORF67; ORF83; ORF84; ORF86; ORF87; ORF125; ORF143; ORF144; ORF179; ORF182; ORF184; ORF185; ORF187; ORF221; ORF252; ORF254;; ORF278; ORF279; ORF387; ORF388; ORF397; ORF1048; ORF1049; ORF1050; ORF1128; ORF1130; ORF1131 and one of their representative fragments.

Also forming part of the invention are polypeptides encoded by the polynucleotides of

20 the invention, as well as fusion polypeptides comprising such polypeptides. In one embodiment, the polypeptides and fusion polypeptides immunoreact with seropositive serum of an individual infected with *Chlamydia pneumoniae*. For example, described below, are polypeptide sequences exhibiting particularly preferable characteristics. For each group of preferred polypeptides described below, it is to be understood that in addition to the individual polypeptides listed, in instances wherein such

25 polypeptides are encoded as part of "combined" ORFs, such "combined" polypeptides are also to be included within the preferred group.

The subject of the invention is also a polypeptide according to the invention, characterized in that it is a polypeptide of the cellular envelope, preferably of the outer cellular envelope, of *Chlamydia pneumoniae* or one of its representative fragments.   According to the

30 invention, the said polypeptide is preferably chosen from the polypeptides having the following sequences:

SEQ ID No. 15; SEQ ID No. 25; SEQ ID No. 26; SEQ ID No. 27; SEQ ID No. 28; SEQ ID No. 29; SEQ ID No. 30; SEQ ID No. 31; SEQ ID No. 32; SEQ ID No. 33; SEQ ID No. 35; SEQ ID No. 68; SEQ ID No. 124; SEQ ID No. 275; SEQ ID No. 291; SEQ ID No. 294; SEQ ID No. 327; SEQ ID

35 No. 342; SEQ ID No. 364; SEQ ID No. 374; SEQ ID No. 380; SEQ ID No. 414; SEQ ID No. 439; SEQ ID No. 466; SEQ ID No. 467; SEQ ID No. 468; SEQ ID No. 469; SEQ ID No. 470; SEQ ID No. 472; SEQ ID No. 474; SEQ ID No. 476; SEQ ID No. 477; SEQ ID No. 478; SEQ ID No. 479;

SEQ ID No. 480; SEQ ID No. 482; SEQ ID No. 485; SEQ ID No. 500; SEQ ID No. 501; SEQ ID No. 503; SEQ ID No. 504; SEQ ID No. 505; SEQ ID No. 506; SEQ ID No. 520; SEQ ID No. 578; SEQ ID No. 580; SEQ ID No. 581; SEQ ID No. 595; SEQ ID No. 596; SEQ ID No. 597; SEQ ID No. 737; SEQ ID No. 830; SEQ ID No. 834; SEQ ID No. 836; SEQ ID No. 893; SEQ ID
5   No. 917; SEQ ID No. 932; SEQ ID No. 976; SEQ ID No. 1035; SEQ ID No. 1045; SEQ ID No. 1090 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* transmembrane polypeptide or one of its representative fragments, having between 1 and 3 transmembrane domains, and in that it is chosen
10   from the polypeptides having the following sequences:

SEQ ID No. 2; SEQ ID No. 3; SEQ ID No. 6; SEQ ID No. 9; SEQ ID No. 10; SEQ ID No. 11; SEQ ID No. 13; SEQ ID No. 14; SEQ ID No. 16; SEQ ID No. 18; SEQ ID No. 19; SEQ ID No. 20; SEQ ID No. 21; SEQ ID No. 22; SEQ ID No. 25; SEQ ID No. 27; SEQ ID No. 28; SEQ ID No. 29; SEQ ID No. 30; SEQ ID No. 31; SEQ ID No. 32; SEQ ID No. 33; SEQ ID No. 34;
15   SEQ ID No. 35; SEQ ID No. 37; SEQ ID No. 39; SEQ ID No. 41; SEQ ID No. 42; SEQ ID No. 44; SEQ ID No. 45; SEQ ID No. 46; SEQ ID No. 47; SEQ ID No. 48; SEQ ID No. 49; SEQ ID No. 50; SEQ ID No. 53; SEQ ID No. 54; SEQ ID No. 56; SEQ ID No. 57; SEQ ID No. 59; SEQ ID No. 60; SEQ ID No. 61; SEQ ID No. 62; SEQ ID No. 63; SEQ ID No. 64; SEQ ID No. 65; SEQ ID No. 66; SEQ ID No. 69;; SEQ ID No. 72; SEQ ID No. 73; SEQ ID
20   No. 74; SEQ ID No. 76; SEQ ID No. 77; SEQ ID No. 78; SEQ ID No. 79; SEQ ID No. 80; SEQ ID No. 82; SEQ ID No. 84; SEQ ID No. 85; SEQ ID No. 86; SEQ ID No. 88; SEQ ID No. 89; SEQ ID No. 90; SEQ ID No. 91; SEQ ID No. 92; SEQ ID No. 93; SEQ ID No. 95; SEQ ID No. 96; SEQ ID No. 98; SEQ ID No. 99; SEQ ID No. 100; SEQ ID No. 101; SEQ ID No. 102; SEQ ID No. 103; SEQ ID No. 104; SEQ ID No. 105; SEQ ID No. 106; SEQ ID No. 107;
25   SEQ ID No. 108; SEQ ID No. 114; SEQ ID No. 117; SEQ ID No. 118; SEQ ID No. 122; SEQ ID No. 123; SEQ ID No. 124; SEQ ID No. 125; SEQ ID No. 129; SEQ ID No. 130; SEQ ID No. 131; SEQ ID No. 132; SEQ ID No. 133; SEQ ID No. 134; SEQ ID No. 135; SEQ ID No. 137; SEQ ID No. 138; SEQ ID No. 139; SEQ ID No. 140; SEQ ID No. 141; SEQ ID No. 142; SEQ ID No. 143; SEQ ID No. 145; SEQ ID No. 146; SEQ ID No. 147; SEQ ID No. 150; SEQ ID No. 151; SEQ ID
30   No. 152; SEQ ID No. 156; SEQ ID No. 157; SEQ ID No. 158; SEQ ID No. 159; SEQ ID No. 160; SEQ ID No. 161; SEQ ID No. 162; SEQ ID No. 164; SEQ ID No. 166; SEQ ID No. 167; SEQ ID No. 170; SEQ ID No. 173; SEQ ID No. 175; SEQ ID No. 176; SEQ ID No. 178; SEQ ID No. 179; SEQ ID No. 180; SEQ ID No. 182; SEQ ID No. 183; SEQ ID No. 184; SEQ ID No. 185; SEQ ID No. 186; SEQ ID No. 187; SEQ ID No. 188; SEQ ID No. 189; SEQ ID No. 190; SEQ ID No. 191;
35   SEQ ID No. 192; SEQ ID No. 194; SEQ ID No. 195; SEQ ID No. 196; SEQ ID No. 197; SEQ ID No. 198; SEQ ID No. 199; SEQ ID No. 200; SEQ ID No. 201; SEQ ID No. 202; SEQ ID No. 205; SEQ ID No. 207; SEQ ID No. 208; SEQ ID No. 209; SEQ ID No. 210; SEQ ID No. 212; SEQ ID

No. 215; SEQ ID No. 219; SEQ ID No. 220; SEQ ID No. 224; SEQ ID No. 226; SEQ ID

No. 227; SEQ ID No. 228; SEQ ID No. 231; SEQ ID No. 232; SEQ ID No. 233; SEQ ID No. 234;

SEQ ID No. 235; SEQ ID No. 236; SEQ ID No. 238; SEQ ID No. 239; SEQ ID No. 240; SEQ ID

No. 241; SEQ ID No. 242; SEQ ID No. 244; SEQ ID No. 247; SEQ ID No. 251; SEQ ID No. 252;

5   SEQ ID No. 253; SEQ ID No. 255; SEQ ID No. 256; SEQ ID No. 257; SEQ ID No. 258; SEQ ID

No. 260; SEQ ID No. 262; SEQ ID No. 263; SEQ ID No. 266; SEQ ID No. 267; SEQ ID No. 268;

SEQ ID No. 269; SEQ ID No. 270; SEQ ID No. 273; SEQ ID No. 274; SEQ ID No. 276; SEQ ID

No. 278; SEQ ID No. 279; SEQ ID No. 280; SEQ ID No. 281; SEQ ID No. 282; SEQ ID No. 283;

SEQ ID No. 284; SEQ ID No. 286; SEQ ID No. 287; SEQ ID No. 289; SEQ ID No. 290; SEQ ID

10 No. 291; SEQ ID No. 293; SEQ ID No. 294; SEQ ID No. 297; SEQ ID No. 304; SEQ ID No. 305;

SEQ ID No. 307; SEQ ID No. 308; SEQ ID No. 309; SEQ ID No. 310; SEQ ID No. 311; SEQ ID

No. 313; SEQ ID No. 314; SEQ ID No. 315; SEQ ID No. 316; SEQ ID No. 318; SEQ ID No. 319;

SEQ ID No. 320; SEQ ID No. 321; SEQ ID No. 322; SEQ ID No. 323; SEQ ID No. 324; SEQ ID

No. 325; SEQ ID No. 326; SEQ ID No. 331; SEQ ID No. 332; SEQ ID No. 336; SEQ ID No. 338;

15 SEQ ID No. 339; SEQ ID No. 341; SEQ ID No. 344; SEQ ID No. 345; SEQ ID No. 346; SEQ ID

No. 350; SEQ ID No. 352; SEQ ID No. 353; SEQ ID No. 356; SEQ ID No. 357; SEQ ID No. 358;

SEQ ID No. 359; SEQ ID No. 360; SEQ ID No. 362; SEQ ID No. 365; SEQ ID No. 366; SEQ ID

No. 367; SEQ ID No. 370; SEQ ID No. 372; SEQ ID No. 373; SEQ ID No. 376; SEQ ID No. 377;

SEQ ID No. 378; SEQ ID No. 379; SEQ ID No. 381; SEQ ID No. 382; SEQ ID No. 383; SEQ ID

20 No. 384; SEQ ID No. 385; SEQ ID No. 386; SEQ ID No. 387; SEQ ID No. 390; SEQ ID No. 392;

SEQ ID No. 393; SEQ ID No. 394; SEQ ID No. 396; SEQ ID No. 398; SEQ ID No. 399; SEQ ID

No. 400; SEQ ID No. 404; SEQ ID No. 408; SEQ ID No. 410; SEQ ID No. 411; SEQ ID No. 413;

SEQ ID No. 416; SEQ ID No. 417; SEQ ID No. 418; SEQ ID No. 420; SEQ ID No. 422; SEQ ID

No. 424; SEQ ID No. 427; SEQ ID No. 428; SEQ ID No. 429; SEQ ID No. 430; SEQ ID No. 431;

25 SEQ ID No. 433; SEQ ID No. 434; SEQ ID No. 437; SEQ ID No. 440; SEQ ID No. 441; SEQ ID

No. 442; SEQ ID No. 443; SEQ ID No. 444; SEQ ID No. 445; SEQ ID No. 447; SEQ ID No. 450;

SEQ ID No. 451; SEQ ID No. 452; SEQ ID No. 455; SEQ ID No. 456; SEQ ID No. 459; SEQ ID

No. 460; SEQ ID No. 461; SEQ ID No. 462; SEQ ID No. 463; SEQ ID No. 464; SEQ ID No. 465;

SEQ ID No. 467; SEQ ID No. 469; SEQ ID No. 471; SEQ ID No. 474; SEQ ID No. 475; SEQ ID

30 No. 476; SEQ ID No. 477; SEQ ID No. 479; SEQ ID No. 482; SEQ ID No. 483; SEQ ID No. 484;

SEQ ID No. 485; SEQ ID No. 486; SEQ ID No. 487; SEQ ID No. 488; SEQ ID No. 491; SEQ ID

No. 493; SEQ ID No. 494; SEQ ID No. 497; SEQ ID No. 498; SEQ ID No. 499; SEQ ID No. 503;

SEQ ID No. 508; SEQ ID No. 509; SEQ ID No. 510; SEQ ID No. 512; SEQ ID No. 514; SEQ ID

No. 515; SEQ ID No. 516; SEQ ID No. 517; SEQ ID No. 518; SEQ ID No. 520; SEQ ID No. 521;

35 SEQ ID No. 523; SEQ ID No. 525; SEQ ID No. 527; SEQ ID No. 528; SEQ ID No. 529; SEQ ID

No. 530; SEQ ID No. 531; SEQ ID No. 533; SEQ ID No. 534; SEQ ID No. 535; SEQ ID No. 536;

SEQ ID No. 537; SEQ ID No. 540; SEQ ID No. 541; SEQ ID No. 543; SEQ ID No. 544; SEQ ID

No. 545; SEQ ID No. 546; SEQ ID No. 548; SEQ ID No. 549; SEQ ID No. 551; SEQ ID No. 553; SEQ ID No. 554; SEQ ID No. 555; SEQ ID No. 556; SEQ ID No. 557; SEQ ID No. 558; SEQ ID No. 559; SEQ ID No. 560; SEQ ID No. 562; SEQ ID No. 563; SEQ ID No. 564; SEQ ID No. 565; SEQ ID No. 566; SEQ ID No. 569; SEQ ID No. 571; SEQ ID No. 573; SEQ ID No. 576;

5   SEQ ID No. 577; SEQ ID No. 581; SEQ ID No. 583; SEQ ID No. 584; SEQ ID No. 585; SEQ ID No. 586; SEQ ID No. 588; SEQ ID No. 591; SEQ ID No. 592; SEQ ID No. 594; SEQ ID No. 595; SEQ ID No. 596; SEQ ID No. 597; SEQ ID No. 599; SEQ ID No. 600; SEQ ID No. 603; SEQ ID No. 605; SEQ ID No. 608; SEQ ID No. 614; SEQ ID No. 615; SEQ ID No. 620; SEQ ID No. 621; SEQ ID No. 622; SEQ ID No. 623; SEQ ID No. 624; SEQ ID No. 625; SEQ ID No. 629; SEQ ID

10 No. 630; SEQ ID No. 631; SEQ ID No. 633; SEQ ID No. 634; SEQ ID No. 637; SEQ ID No. 642; SEQ ID No. 644; SEQ ID No. 645; SEQ ID No. 647; SEQ ID No. 648; SEQ ID No. 652; SEQ ID No. 654; SEQ ID No. 655; SEQ ID No. 657; SEQ ID No. 658; SEQ ID No. 659; SEQ ID No. 660; SEQ ID No. 661; SEQ ID No. 664; SEQ ID No. 665; SEQ ID No. 666; SEQ ID No. 667; SEQ ID No. 670; SEQ ID No. 671; SEQ ID No. 672; SEQ ID No. 673; SEQ ID No. 674; SEQ ID No. 676;

15 SEQ ID No. 679; SEQ ID No. 681; SEQ ID No. 684; SEQ ID No. 687; SEQ ID No. 688; SEQ ID No. 689; SEQ ID No. 690; SEQ ID No. 693; SEQ ID No. 694; SEQ ID No. 695; SEQ ID No. 696; SEQ ID No. 697; SEQ ID No. 698; SEQ ID No. 699; SEQ ID No. 700; SEQ ID No. 701; SEQ ID No. 703; SEQ ID No. 705; SEQ ID No. 706; SEQ ID No. 707; SEQ ID No. 708; SEQ ID No. 710; SEQ ID No. 712; SEQ ID No. 715; SEQ ID No. 716; SEQ ID No. 717; SEQ ID No. 718; SEQ ID

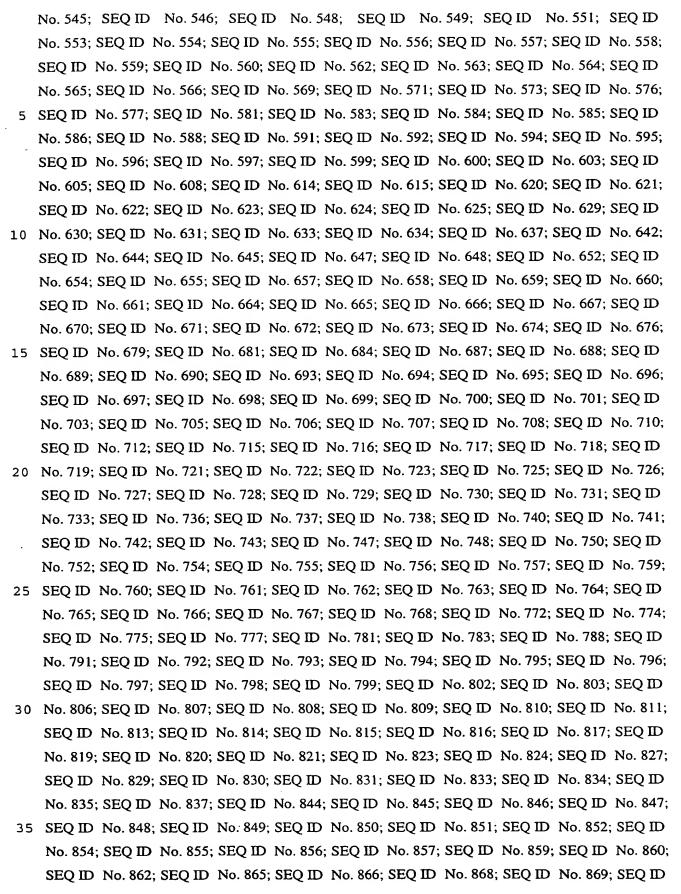20 No. 719; SEQ ID No. 721; SEQ ID No. 722; SEQ ID No. 723; SEQ ID No. 725; SEQ ID No. 726; SEQ ID No. 727; SEQ ID No. 728; SEQ ID No. 729; SEQ ID No. 730; SEQ ID No. 731; SEQ ID No. 733; SEQ ID No. 736; SEQ ID No. 737; SEQ ID No. 738; SEQ ID No. 740; SEQ ID No. 741; SEQ ID No. 742; SEQ ID No. 743; SEQ ID No. 747; SEQ ID No. 748; SEQ ID No. 750; SEQ ID No. 752; SEQ ID No. 754; SEQ ID No. 755; SEQ ID No. 756; SEQ ID No. 757; SEQ ID No. 759;

25 SEQ ID No. 760; SEQ ID No. 761; SEQ ID No. 762; SEQ ID No. 763; SEQ ID No. 764; SEQ ID No. 765; SEQ ID No. 766; SEQ ID No. 767; SEQ ID No. 768; SEQ ID No. 772; SEQ ID No. 774; SEQ ID No. 775; SEQ ID No. 777; SEQ ID No. 781; SEQ ID No. 783; SEQ ID No. 788; SEQ ID No. 791; SEQ ID No. 792; SEQ ID No. 793; SEQ ID No. 794; SEQ ID No. 795; SEQ ID No. 796; SEQ ID No. 797; SEQ ID No. 798; SEQ ID No. 799; SEQ ID No. 802; SEQ ID No. 803; SEQ ID

30 No. 806; SEQ ID No. 807; SEQ ID No. 808; SEQ ID No. 809; SEQ ID No. 810; SEQ ID No. 811; SEQ ID No. 813; SEQ ID No. 814; SEQ ID No. 815; SEQ ID No. 816; SEQ ID No. 817; SEQ ID No. 819; SEQ ID No. 820; SEQ ID No. 821; SEQ ID No. 823; SEQ ID No. 824; SEQ ID No. 827; SEQ ID No. 829; SEQ ID No. 830; SEQ ID No. 831; SEQ ID No. 833; SEQ ID No. 834; SEQ ID No. 835; SEQ ID No. 837; SEQ ID No. 844; SEQ ID No. 845; SEQ ID No. 846; SEQ ID No. 847;

35 SEQ ID No. 848; SEQ ID No. 849; SEQ ID No. 850; SEQ ID No. 851; SEQ ID No. 852; SEQ ID No. 854; SEQ ID No. 855; SEQ ID No. 856; SEQ ID No. 857; SEQ ID No. 859; SEQ ID No. 860; SEQ ID No. 862; SEQ ID No. 865; SEQ ID No. 866; SEQ ID No. 868; SEQ ID No. 869; SEQ ID

No. 870; SEQ ID No. 871; SEQ ID No. 872; SEQ ID No. 874; SEQ ID No. 877; SEQ ID No. 878; SEQ ID No. 879; SEQ ID No. 880; SEQ ID No. 881; SEQ ID No. 882; SEQ ID No. 884; SEQ ID No. 885; SEQ ID No. 888; SEQ ID No. 889; SEQ ID No. 890; SEQ ID No. 891; SEQ ID No. 892; SEQ ID No. 894; SEQ ID No. 895; SEQ ID No. 896; SEQ ID No. 897; SEQ ID No. 899;

5 SEQ ID No. 900; SEQ ID No. 902; SEQ ID No. 903; SEQ ID No. 904; SEQ ID No. 905; SEQ ID No. 909; SEQ ID No. 910; SEQ ID No. 912; SEQ ID No. 913; SEQ ID No. 914; SEQ ID No. 915; SEQ ID No. 917; SEQ ID No. 918; SEQ ID No. 919; SEQ ID No. 921; SEQ ID No. 923; SEQ ID No. 924; SEQ ID No. 926; SEQ ID No. 927; SEQ ID No. 928; SEQ ID No. 929; SEQ ID No. 930; SEQ ID No. 931; SEQ ID No. 937; SEQ ID No. 938; SEQ ID No. 939; SEQ ID No. 941; SEQ ID

10 No. 943; SEQ ID No. 948; SEQ ID No. 951; SEQ ID No. 952; SEQ ID No. 953; SEQ ID No. 958; SEQ ID No. 960; SEQ ID No. 963; SEQ ID No. 964; SEQ ID No. 965; SEQ ID No. 968; SEQ ID No. 970; SEQ ID No. 974; SEQ ID No. 975; SEQ ID No. 977; SEQ ID No. 979; SEQ ID No. 980; SEQ ID No. 981; SEQ ID No. 983; SEQ ID No. 984; SEQ ID No. 985; SEQ ID No. 987; SEQ ID No. 989; SEQ ID No. 992; SEQ ID No. 993; SEQ ID No. 997; SEQ ID No. 998; SEQ ID No. 999;

15 SEQ ID No. 1001; SEQ ID No. 1002; SEQ ID No. 1004; SEQ ID No. 1005; SEQ ID No. 1009; SEQ ID No. 1013; SEQ ID No. 1014; SEQ ID No. 1015; SEQ ID No. 1016; SEQ ID No. 1019; SEQ ID No. 1021; SEQ ID No. 1023; SEQ ID No. 1024; SEQ ID No. 1029; SEQ ID No. 1031; SEQ ID No. 1033; SEQ ID No. 1034; SEQ ID No. 1039; SEQ ID No. 1041; SEQ ID No. 1042; SEQ ID No. 1045; SEQ ID No. 1047; SEQ ID No. 1049; SEQ ID No. 1051; SEQ ID No. 1052;

20 SEQ ID No. 1053; SEQ ID No. 1054; SEQ ID No. 1056; SEQ ID No. 1059; SEQ ID No. 1061; SEQ ID No. 1062; SEQ ID No. 1063; SEQ ID No. 1064; SEQ ID No. 1065; SEQ ID No. 1067; SEQ ID No. 1075; SEQ ID No. 1077; SEQ ID No. 1078; SEQ ID No. 1079; SEQ ID No. 1080; SEQ ID No. 1081; SEQ ID No. 1089; SEQ ID No. 1095; SEQ ID No. 1097; SEQ ID No. 1098; SEQ ID No. 1099; SEQ ID No. 1101; SEQ ID No. 1102; SEQ ID No. 1103; SEQ ID No. 1106;

25 SEQ ID No. 1107; SEQ ID No. 1108; SEQ ID No. 1109; SEQ ID No. 1110; SEQ ID No. 1113; SEQ ID No. 1116; SEQ ID No. 1118; SEQ ID No. 1119; SEQ ID No. 1121; SEQ ID No. 1123; SEQ ID No. 1124; SEQ ID No. 1126; SEQ ID No. 1128; SEQ ID No. 1130; SEQ ID No. 1131; SEQ ID No. 1133; SEQ ID No. 1134; SEQ ID No. 1136; SEQ ID No. 1137 and one of their representative fragments.

30   Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* transmembrane polypeptide or one of its respective fragments, having between 4 and 6 transmembrane domains, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 5; SEQ ID No. 7; SEQ ID No. 8; SEQ ID No. 15; SEQ ID No. 36; SEQ ID No. 38;

35 SEQ ID No. 51; SEQ ID No. 55; SEQ ID No. 58; SEQ ID No. 67; SEQ ID No. 70; SEQ ID No. 81; SEQ ID No. 97; SEQ ID No. 110; SEQ ID No. 111; SEQ ID No. 115; SEQ ID No. 119; SEQ ID No. 126; SEQ ID No. 128; SEQ ID No. 148; SEQ ID No. 155; SEQ ID No. 163; SEQ ID

No. 165; SEQ ID No. 168; SEQ ID No. 169; SEQ ID No. 171; SEQ ID No. 172; SEQ ID No. 174; SEQ ID No. 177; SEQ ID No. 181; SEQ ID No. 193; SEQ ID No. 203; SEQ ID No. 213; SEQ ID No. 214; SEQ ID No. 216; SEQ ID No. 217; SEQ ID No. 221; SEQ ID No. 222; SEQ ID No. 225; SEQ ID No. 229; SEQ ID No. 243; SEQ ID No. 246; SEQ ID No. 248; SEQ ID No. 254;

5 SEQ ID No. 261; SEQ ID No. 285; SEQ ID No. 288; SEQ ID No. 292; SEQ ID No. 296; SEQ ID No. 298; SEQ ID No. 299; SEQ ID No. 301; SEQ ID No. 303; SEQ ID No. 317; SEQ ID No. 328; SEQ ID No. 329; SEQ ID No. 351; SEQ ID No. 354; SEQ ID No. 355; SEQ ID No. 364; SEQ ID No. 371; SEQ ID No. 374; SEQ ID No. 375; SEQ ID No. 391; SEQ ID No. 395; SEQ ID No. 401; SEQ ID No. 403; SEQ ID No. 405; SEQ ID No. 409; SEQ ID No. 414; SEQ ID No. 419; SEQ ID

10 No. 421; SEQ ID No. 423; SEQ ID No. 425; SEQ ID No. 438; SEQ ID No. 448; SEQ ID No. 453; SEQ ID No. 458; SEQ ID No. 466; SEQ ID No. 468; SEQ ID No. 470; SEQ ID No. 480; SEQ ID No. 489; SEQ ID No. 490; SEQ ID No. 496; SEQ ID No. 501; SEQ ID No. 504; SEQ ID No. 505; SEQ ID No. 506; SEQ ID No. 511; SEQ ID No. 513; SEQ ID No. 519; SEQ ID No. 526; SEQ ID No. 532; SEQ ID No. 538; SEQ ID No. 539; SEQ ID No. 547; SEQ ID No. 550; SEQ ID No. 561;

15 SEQ ID No. 568; SEQ ID No. 570; SEQ ID No. 574; SEQ ID No. 578; SEQ ID No. 579; SEQ ID No. 580; SEQ ID No. 582; SEQ ID No. 589; SEQ ID No. 593; SEQ ID No. 598; SEQ ID No. 601; SEQ ID No. 604; SEQ ID No. 610; SEQ ID No. 613; SEQ ID No. 617; SEQ ID No. 626; SEQ ID No. 632; SEQ ID No. 635; SEQ ID No. 638; SEQ ID No. 640; SEQ ID No. 641; SEQ ID No. 646; SEQ ID No. 649; SEQ ID No. 650; SEQ ID No. 651; SEQ ID No. 686; SEQ ID No. 711; SEQ ID

20 No. 724; SEQ ID No. 732; SEQ ID No. 734; SEQ ID No. 744; SEQ ID No. 745; SEQ ID No. 749; SEQ ID No. 751; SEQ ID No. 769; SEQ ID No. 770; SEQ ID No. 771; SEQ ID No. 773; SEQ ID No. 776; SEQ ID No. 779; SEQ ID No. 780; SEQ ID No. 785; SEQ ID No. 787; SEQ ID No. 789; SEQ ID No. 801; SEQ ID No. 805; SEQ ID No. 812; SEQ ID No. 822; SEQ ID No. 825; SEQ ID No. 826; SEQ ID No. 839; SEQ ID No. 841; SEQ ID No. 843; SEQ ID No. 853; SEQ ID No. 861;

25 SEQ ID No. 875; SEQ ID No. 876; SEQ ID No. 886; SEQ ID No. 893; SEQ ID No. 898; SEQ ID No. 906; SEQ ID No. 907; SEQ ID No. 908; SEQ ID No. 920; SEQ ID No. 922; SEQ ID No. 925; SEQ ID No. 933; SEQ ID No. 935; SEQ ID No. 936; SEQ ID No. 944; SEQ ID No. 946; SEQ ID No. 947; SEQ ID No. 954; SEQ ID No. 959; SEQ ID No. 961; SEQ ID No. 966; SEQ ID No. 967; SEQ ID No. 972; SEQ ID No. 978; SEQ ID No. 995; SEQ ID No. 996; SEQ ID No. 1000; SEQ ID

30 No. 1003; SEQ ID No. 1010; SEQ ID No. 1011; SEQ ID No. 1012; SEQ ID No. 1017; SEQ ID No. 1020; SEQ ID No. 1030; SEQ ID No. 1036; SEQ ID No. 1038; SEQ ID No. 1043; SEQ ID No. 1046; SEQ ID No. 1048; SEQ ID No. 1050; SEQ ID No. 1058; SEQ ID No. 1071; SEQ ID No. 1073; SEQ ID No. 1084; SEQ ID No. 1085; SEQ ID No. 1086; SEQ ID No. 1087; SEQ ID No. 1091; SEQ ID No. 1092; SEQ ID No. 1094; SEQ ID No. 1096; SEQ ID No. 1100; SEQ ID

35 No. 1104; SEQ ID No. 1111; SEQ ID No. 1112; SEQ ID No. 1114; SEQ ID No. 1117; SEQ ID No. 1122; SEQ ID No. 1125 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention,

characterized in that it is a *Chlamydia pneumoniae* transmembrane polypeptide or one of its representative fragments, having at least 7 transmembrane domains, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 17; SEQ ID No. 52; SEQ ID No. 68; SEQ ID No. 83; SEQ ID No. 87; SEQ ID No. 109;

5   SEQ ID No. 112; SEQ ID No. 113; SEQ ID No. 120; SEQ ID No. 121; SEQ ID No. 127; SEQ ID No. 153; SEQ ID No. 204; SEQ ID No. 211; SEQ ID No. 218; SEQ ID No. 223; SEQ ID No. 275; SEQ ID No. 277; SEQ ID No. 295; SEQ ID No. 300; SEQ ID No. 302; SEQ ID No. 306; SEQ ID No. 327; SEQ ID No. 335; SEQ ID No. 342; SEQ ID No. 343; SEQ ID No. 347; SEQ ID No. 349; SEQ ID No. 361; SEQ ID No. 363; SEQ ID No. 369; SEQ ID No. 380; SEQ ID No. 388; SEQ ID

10   No. 389; SEQ ID No. 397; SEQ ID No. 415; SEQ ID No. 432; SEQ ID No. 439; SEQ ID No. 446; SEQ ID No. 449; SEQ ID No. 472; SEQ ID No. 478; SEQ ID No. 500; SEQ ID No. 522; SEQ ID No. 524; SEQ ID No. 567; SEQ ID No. 575; SEQ ID No. 602; SEQ ID No. 606; SEQ ID No. 609; SEQ ID No. 636; SEQ ID No. 639; SEQ ID No. 643; SEQ ID No. 653; SEQ ID No. 668; SEQ ID No. 692; SEQ ID No. 702; SEQ ID No. 704; SEQ ID No. 713; SEQ ID No. 720; SEQ ID No. 778;

15   SEQ ID No. 784; SEQ ID No. 800; SEQ ID No. 836; SEQ ID No. 838; SEQ ID No. 842; SEQ ID No. 864; SEQ ID No. 867; SEQ ID No. 883; SEQ ID No. 901; SEQ ID No. 916; SEQ ID No. 932; SEQ ID No. 934; SEQ ID No. 940; SEQ ID No. 942; SEQ ID No. 950; SEQ ID No. 956; SEQ ID No. 971; SEQ ID No. 973; SEQ ID No. 976; SEQ ID No. 988; SEQ ID No. 994; SEQ ID No. 1018; SEQ ID No. 1028; SEQ ID No. 1035; SEQ ID No. 1037; SEQ ID No. 1044; SEQ ID No. 1055;

20   SEQ ID No. 1057; SEQ ID No. 1068; SEQ ID No. 1069; SEQ ID No. 1070; SEQ ID No. 1072; SEQ ID No. 1082; SEQ ID No. 1088; SEQ ID No. 1105; SEQ ID No. 1132; SEQ ID No. 1135 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* surface exposed polypeptide or one of its representative fragments, and in that

25   it is chosen from the polypeptides having the following sequences:

SEQ ID No. 15, SEQ ID No. 25, SEQ ID No. 26, SEQ ID No. 27, SEQ ID No. 28, SEQ ID No. 29, SEQ ID No. 30, SEQ ID No. 31, SEQ ID No. 32, SEQ ID No. 33, SEQ ID No. 35, SEQ ID No. 36, SEQ ID No. 1257, SEQ ID No. 280, SEQ ID No. 291, SEQ ID No. 314, SEQ ID No. 354, SEQ ID No. 380, SEQ ID No. 1266, SEQ ID No. 466, SEQ ID No. 467, SEQ ID No. 468, SEQ ID No. 469,

30   SEQ ID No. 470, SEQ ID No. 472, SEQ ID No. 474, SEQ ID No. 476, SEQ ID No. 477, SEQ ID No. 478, SEQ ID No. 479, SEQ ID No. 480, SEQ ID No. 482, SEQ ID No. 483, SEQ ID No. 485, SEQ ID No. 486, SEQ ID No. 500, SEQ ID No. 501, SEQ ID No. 503, SEQ ID No. 504, SEQ ID No. 505, SEQ ID No. 506, SEQ ID No. 507, SEQ ID No. 1268, SEQ ID No. 1269, SEQ ID No. 543, SEQ ID No. 544, SEQ ID No. 578, SEQ ID No. 579, SEQ ID No. 580, SEQ ID No. 581, SEQ ID No. 595,

35   SEQ ID No. 596, SEQ ID No. 597, SEQ ID No. 1271, SEQ ID No. 633, SEQ ID No. 637, SEQ ID No. 699, SEQ ID No. 706, SEQ ID No. 737, SEQ ID No. 744, SEQ ID No. 1273, SEQ ID No. 751, SEQ ID No. 775, SEQ ID No. 776, SEQ ID No. 777, SEQ ID No. 793, SEQ ID No. 815, SEQ ID No.

830, SEQ ID No. 1221, SEQ ID No. 849, SEQ ID No. 851, SEQ ID No. 852, SEQ ID No. 874, SEQ ID No. 891, SEQ ID No. 922, SEQ ID No. 940, SEQ ID No. 1231, SEQ ID No. 1281, SEQ ID No. 1035, SEQ ID No. 1079, SEQ ID No. 1087, SEQ ID No. 1108, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* lipoprotein or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 3, SEQ ID No. 10, SEQ ID No. 11, SEQ ID No. 16, SEQ ID No. 1254, SEQ ID No. 1255, SEQ ID No. 38, SEQ ID No. 1256, SEQ ID No. 62, SEQ ID No. 85, SEQ ID No. 1258, SEQ ID No. 115, SEQ ID No. 1151, SEQ ID No. 151, SEQ ID No. 1259, SEQ ID No. 173, SEQ ID No. 1261, SEQ ID No. 186, SEQ ID No. 194, SEQ ID No. 205, SEQ ID No. 214, SEQ ID No. 216, SEQ ID No. 217, SEQ ID No. 238, SEQ ID No. 1177, SEQ ID No. 280, SEQ ID No. 291, SEQ ID No. 317, SEQ ID No. 327, SEQ ID No. 354, SEQ ID No. 364, SEQ ID No. 367, SEQ ID No. 414, SEQ ID No. 432, SEQ ID No. 1192, SEQ ID No. 460, SEQ ID No. 1267, SEQ ID No. 1268, SEQ ID No. 520, SEQ ID No. 536, SEQ ID No. 1270, SEQ ID No. 576, SEQ ID No. 597, SEQ ID No. 603, SEQ ID No. 609, SEQ ID No. 637, SEQ ID No. 1272, SEQ ID No. 652, SEQ ID No. 1213, SEQ ID No. 699, SEQ ID No. 705, SEQ ID No. 706, SEQ ID No. 708, SEQ ID No. 711, SEQ ID No. 727, SEQ ID No. 1274, SEQ ID No. 800, SEQ ID No. 814, SEQ ID No. 825, SEQ ID No. 829, SEQ ID No. 830, SEQ ID No. 831, SEQ ID No. 844, SEQ ID No. 849, SEQ ID No. 1275, SEQ ID No. 1276, SEQ ID No. 1277, SEQ ID No. 872, SEQ ID No. 878, SEQ ID No. 880, SEQ ID No. 891, SEQ ID No. 892, SEQ ID No. 1278, SEQ ID No. 1279, SEQ ID No. 1280, SEQ ID No. 941, SEQ ID No. 942, SEQ ID No. 1282, SEQ ID No. 1283, SEQ ID No. 952, SEQ ID No. 988, SEQ ID No. 998, SEQ ID No. 1009, SEQ ID No. 1285, SEQ ID No. 1235, SEQ ID No. 1028, SEQ ID No. 1056, SEQ ID No. 1070, SEQ ID No. 1287, SEQ ID No. 1087, SEQ ID No. 1288, SEQ ID No. 1289, SEQ ID No. 1098, SEQ ID No. 1246, SEQ ID No. 1291, SEQ ID No. 1108, SEQ ID No. 1109, SEQ ID No. 1112, SEQ ID No. 1133, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* polypeptide involved in lipopolysaccharide (LPS) biosynthesis, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 316, SEQ ID No. 564, SEQ ID No. 610, SEQ ID No. 647, SEQ ID No. 1211, SEQ ID No. 688, SEQ ID No. 924, and one of their representative fragments.

Preferably, the invention relates to additional LPS-related polypeptides according to the invention, in that it is:

(a) a *Chlamydia pneumoniae* KDO (3-deoxy-D-manno-octylosonic acid)-related polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 177, SEQ ID No. 1156, SEQ ID No. 245, SEQ ID No. 767, and one of their representative fragments;

(b) a *Chlamydia pneumoniae* phosphomannomutase-related polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 74, and its representative fragment;

(c) a *Chlamydia pneumoniae* phosphoglucomutase-related polypeptide or one of its
5 representative fragments, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 1286, SEQ ID No. 1039, and its representative fragment; and

(d) a *Chlamydia pneumoniae* lipid A component-related polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 689, SEQ ID No. 690, SEQ ID No. 691, SEQ ID No. 1037, and one of their
10 representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments that contains an RGD sequence and is also an outer membrane protein, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 468 and its representative fragments.

15   Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments that contains an RGD sequence that shows homology to cds1, cds2, and copN type III virulence loci in *Chlamydia Psitacci*, and in that it is chosen from the polypeptides having the following sequences:
SEQ ID No. 350 and its representative fragments.

20   Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments that is cysteine-rich and contains RGD sequence, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 1290, SEQ ID No. 6846, SEQ ID No. 6848, and one of their representative fragments.

25   Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* outer membrane polypeptide that contains cysteines in their first 30 amino acids and also contain an RGD sequence, and in that it is chosen from the polypeptides having the following sequences:
SEQ ID No. 105, SEQ ID No. 106, SEQ ID No. 114, SEQ ID No. 170, SEQ ID No. 171, SEQ ID No.
30 1264, SEQ ID No. 268, SEQ ID No. 1265, SEQ ID No. 350, SEQ ID No. 393, SEQ ID No. 394, SEQ
ID No. 451, SEQ ID No. 452, SEQ ID No. 453, SEQ ID No. 473, SEQ ID No. 499, SEQ ID No. 515,
SEQ ID No. 519, SEQ ID No. 525, SEQ ID No. 526, SEQ ID No. 538, SEQ ID No. 611, SEQ ID No.
645, SEQ ID No. 686, SEQ ID No. 700, SEQ ID No. 746, SEQ ID No. 755, SEQ ID No. 756, SEQ ID
No. 757, SEQ ID No. 789, SEQ ID No. 814, SEQ ID No. 855, SEQ ID No. 856, SEQ ID No. 878,
35 SEQ ID No. 957, SEQ ID No. 958, SEQ ID No. 989, SEQ ID No. 1290, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a

Chlamydia pneumoniae polypeptide or one of its representative fragments that contains RGD sequences homologous to *Chlamydia trachomatis* polypeptides containing RGD sequences, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 114, SEQ ID No. 468, SEQ ID No. 755, SEQ ID No. 756, SEQ ID No. 757, SEQ ID No.

5 855, SEQ ID No. 856, SEQ ID No. 905, SEQ ID No. 913, SEQ ID No. 914, SEQ ID No. 915, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* Type III and non-Type III secreted polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences:

10 SEQ ID No. 25, SEQ ID No. 28, SEQ ID No. 29, SEQ ID No. 33, SEQ ID No. 308, SEQ ID No. 309, SEQ ID No. 343, SEQ ID No. 344, SEQ ID No. 345, SEQ ID No. 367, SEQ ID No. 414, SEQ ID No. 415, SEQ ID No. 480, SEQ ID No. 550, SEQ ID No. 579, SEQ ID No. 580, SEQ ID No. 581, SEQ ID No. 597, SEQ ID No. 699, SEQ ID No. 744, SEQ ID No. 751, SEQ ID No. 776, SEQ ID No. 866, SEQ ID No. 874, SEQ ID No. 883, SEQ ID No. 884, SEQ ID No. 888, SEQ ID No. 891, SEQ ID No.

15 6845, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* cell wall anchored surface polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 267, SEQ ID No. 271, SEQ ID No. 419, SEQ ID No. 590, SEQ ID No. 932, SEQ ID No.

20 6844, SEQ ID No. 6847, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments not found in *Chlamydia trachomatis* (Blastp $P > e^{-10}$), and in that it is chosen from the polypeptides having the following sequences:

25 SEQ ID No. 7, SEQ ID No. 8, SEQ ID No. 9, SEQ ID No. 16, SEQ ID No. 17, SEQ ID No. 18, SEQ ID No. 19, SEQ ID No. 20, SEQ ID No. 21, SEQ ID No. 22, SEQ ID No. 1254, SEQ ID No. 23, SEQ ID No. 1255, SEQ ID No. 24, SEQ ID No. 1139, SEQ ID No. 1140, SEQ ID No. 46, SEQ ID No. 47, SEQ ID No. 51, SEQ ID No. 60, SEQ ID No. 1256, SEQ ID No. 61, SEQ ID No. 62, SEQ ID No. 63, SEQ ID No. 64, SEQ ID No. 1257, SEQ ID No. 65, SEQ ID No. 66, SEQ ID No. 67, SEQ ID No. 68,

30 SEQ ID No. 1143, SEQ ID No. 1145, SEQ ID No. 83, SEQ ID No. 84, SEQ ID No. 1146, SEQ ID No. 85, SEQ ID No. 86, SEQ ID No. 87, SEQ ID No. 1258, SEQ ID No. 116, SEQ ID No. 117, SEQ ID No. 125, SEQ ID No. 1148, SEQ ID No. 143, SEQ ID No. 1150, SEQ ID No. 1151, SEQ ID No. 144, SEQ ID No. 145, SEQ ID No. 147, SEQ ID No. 148, SEQ ID No. 149, SEQ ID No. 150, SEQ ID No. 152, SEQ ID No. 1259, SEQ ID No. 162, SEQ ID No. 166, SEQ ID No. 1154, SEQ ID No. 167,

35 SEQ ID No. 1261, SEQ ID No. 1156, SEQ ID No. 1157, SEQ ID No. 178, SEQ ID No. 179, SEQ ID No. 1158, SEQ ID No. 182, SEQ ID No. 183, SEQ ID No. 184, SEQ ID No. 185, SEQ ID No. 1159, SEQ ID No. 186, SEQ ID No. 1160, SEQ ID No. 187, SEQ ID No. 188, SEQ ID No. 189, SEQ ID

No. 190, SEQ ID No. 1161, SEQ ID No. 1162, SEQ ID No. 191, SEQ ID No. 192, SEQ ID No. 194, SEQ ID No. 195, SEQ ID No. 1163, SEQ ID No. 196, SEQ ID No. 201, SEQ ID No. 202, SEQ ID No. 209, SEQ ID No. 212, SEQ ID No. 221, SEQ ID No. 224, SEQ ID No. 1167, SEQ ID No. 226, SEQ ID No. 227, SEQ ID No. 228, SEQ ID No. 229, SEQ ID No. 230, SEQ ID No. 231, SEQ ID No.

5   232, SEQ ID No. 1169, SEQ ID No. 1170, SEQ ID No. 1171, SEQ ID No. 234, SEQ ID No. 235, SEQ ID No. 236, SEQ ID No. 1172, SEQ ID No. 243, SEQ ID No. 251, SEQ ID No. 252, SEQ ID No. 1176, SEQ ID No. 253, SEQ ID No. 255, SEQ ID No. 254, SEQ ID No. 256, SEQ ID No. 1177, SEQ ID No. 1178, SEQ ID No. 262, SEQ ID No. 263, SEQ ID No. 1264, SEQ ID No. 278, SEQ ID No. 279, SEQ ID No. 1180, SEQ ID No. 280, SEQ ID No. 290, SEQ ID No. 291, SEQ ID No. 292, SEQ

10   ID No. 296, SEQ ID No. 1181, SEQ ID No. 297, SEQ ID No. 298, SEQ ID No. 300, SEQ ID No. 1265, SEQ ID No. 322, SEQ ID No. 324, SEQ ID No. 325, SEQ ID No. 370, SEQ ID No. 1186, SEQ ID No. 371, SEQ ID No. 372, SEQ ID No. 1187, SEQ ID No. 373, SEQ ID No. 378, SEQ ID No. 1266, SEQ ID No. 382, SEQ ID No. 383, SEQ ID No. 384, SEQ ID No. 385, SEQ ID No. 386, SEQ ID No. 1188, SEQ ID No. 1189, SEQ ID No. 391, SEQ ID No. 392, SEQ ID No. 398, SEQ ID No.

15   400, SEQ ID No. 403, SEQ ID No. 1191, SEQ ID No. 423, SEQ ID No. 435, SEQ ID No. 445, SEQ ID No. 450, SEQ ID No. 1193, SEQ ID No. 456, SEQ ID No. 460, SEQ ID No. 461, SEQ ID No. 465, SEQ ID No. 1196, SEQ ID No. 471, SEQ ID No. 473, SEQ ID No. 475, SEQ ID No. 481, SEQ ID No. 484, SEQ ID No. 487, SEQ ID No. 488, SEQ ID No. 489, SEQ ID No. 490, SEQ ID No. 491, SEQ ID No. 492, SEQ ID No. 493, SEQ ID No. 494, SEQ ID No. 495, SEQ ID No. 496, SEQ ID No.

20   497, SEQ ID No. 498, SEQ ID No. 499, SEQ ID No. 502, SEQ ID No. 1267, SEQ ID No. 1268, SEQ ID No. 508, SEQ ID No. 510, SEQ ID No. 509, SEQ ID No. 512, SEQ ID No. 515, SEQ ID No. 519, SEQ ID No. 1197, SEQ ID No. 521, SEQ ID No. 1198, SEQ ID No. 522, SEQ ID No. 524, SEQ ID No. 528, SEQ ID No. 534, SEQ ID No. 537, SEQ ID No. 1269, SEQ ID No. 1270, SEQ ID No. 548, SEQ ID No. 551, SEQ ID No. 557, SEQ ID No. 1201, SEQ ID No. 1203, SEQ ID No. 562, SEQ ID

25   No. 566, SEQ ID No. 593, SEQ ID No. 595, SEQ ID No. 600, SEQ ID No. 1271, SEQ ID No. 604, SEQ ID No. 611, SEQ ID No. 612, SEQ ID No. 614, SEQ ID No. 616, SEQ ID No. 625, SEQ ID No. 627, SEQ ID No. 628, SEQ ID No. 629, SEQ ID No. 631, SEQ ID No. 641, SEQ ID No. 1272, SEQ ID No. 648, SEQ ID No. 1212, SEQ ID No. 663, SEQ ID No. 685, SEQ ID No. 707, SEQ ID No. 714, SEQ ID No. 715, SEQ ID No. 716, SEQ ID No. 717, SEQ ID No. 722, SEQ ID No. 746, SEQ ID No.

30   1273, SEQ ID No. 761, SEQ ID No. 764, SEQ ID No. 770, SEQ ID No. 1217, SEQ ID No. 783, SEQ ID No. 1274, SEQ ID No. 803, SEQ ID No. 815, SEQ ID No. 1220, SEQ ID No. 835, SEQ ID No. 1221, SEQ ID No. 844, SEQ ID No. 845, SEQ ID No. 846, SEQ ID No. 847, SEQ ID No. 848, SEQ ID No. 849, SEQ ID No. 850, SEQ ID No. 851, SEQ ID No. 1275, SEQ ID No. 852, SEQ ID No. 862, SEQ ID No. 1276, SEQ ID No. 1277, SEQ ID No. 873, SEQ ID No. 1223, SEQ ID No. 892, SEQ ID

35   No. 919, SEQ ID No. 1225, SEQ ID No. 1278, SEQ ID No. 926, SEQ ID No. 1228, SEQ ID No. 1229, SEQ ID No. 1230, SEQ ID No. 1279, SEQ ID No. 1281, SEQ ID No. 1282, SEQ ID No. 1283, SEQ ID No. 948, SEQ ID No. 950, SEQ ID No. 949, SEQ ID No. 951, SEQ ID No. 980, SEQ ID No.

982, SEQ ID No. 1233, SEQ ID No. 999, SEQ ID   No. 1000, SEQ ID No. 1001, SEQ ID No. 1002, SEQ ID No. 1008, SEQ ID No. 1285, SEQ ID No. 1235, SEQ ID No. 1016, SEQ ID No. 1019, SEQ ID No. 1027, SEQ ID No. 1036, SEQ ID No. 1241, SEQ ID No. 1048, SEQ ID No. 1049, SEQ ID No. 1050, SEQ ID No. 1053, SEQ ID No. 1054, SEQ ID No. 1064, SEQ ID No. 1076, SEQ ID No. 1091,

5   SEQ ID No. 1288, SEQ ID No. 1093, SEQ ID No. 1289, SEQ ID No. 1101, SEQ ID No. 1103, SEQ ID No. 1245, SEQ ID No. 1246, SEQ ID No. 1247, SEQ ID No. 1290, SEQ ID No. 1291, SEQ ID No. 1115, SEQ ID No. 1116, SEQ ID No. 1118, SEQ ID No. 1120, SEQ ID No. 1249, SEQ ID No. 1121, SEQ ID No. 1250, SEQ ID No. 1126, SEQ ID No. 1251, SEQ ID No. 1127, SEQ ID No. 1128, SEQ ID No. 1130, SEQ ID No. 1129, SEQ ID No. 1131, SEQ ID No. 1136, SEQ ID No. 1253, SEQ ID No.

10 6844, SEQ ID No. 6846, SEQ ID No. 6847, SEQ ID No. 6848, and one of their representative fragments

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the intermediate metabolism, in particular in the metabolism of sugars and/or of

15 cofactors, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 2; SEQ ID No. 55; SEQ ID No. 56; SEQ ID No. 69; SEQ ID No. 75; SEQ ID No. 80; SEQ ID No. 100; SEQ ID No. 110; SEQ ID No. 114; SEQ ID No. 120; SEQ ID No. 121; SEQ ID No. 157; SEQ ID No. 160; SEQ ID No. 161; SEQ ID No. 172; SEQ ID No. 180; SEQ ID No. 181; SEQ ID No. 198; SEQ ID No. 200; SEQ ID No. 225; SEQ ID No. 248; SEQ ID No. 249; SEQ ID

20 No. 276; SEQ ID No. 277; SEQ ID No. 318; SEQ ID No. 319; SEQ ID No. 320; SEQ ID No. 323; SEQ ID No. 331; SEQ ID No. 347; SEQ ID No. 375; SEQ ID No. 376; SEQ ID No. 381; SEQ ID No. 393; SEQ ID No. 394; SEQ ID No. 395; SEQ ID No. 396; SEQ ID No. 409; SEQ ID No. 446; SEQ ID No. 447; SEQ ID No. 448; SEQ ID No. 449; SEQ ID No. 513; SEQ ID No. 516; SEQ ID No. 571; SEQ ID No. 647; SEQ ID No. 662; SEQ ID No. 697; SEQ ID No. 718; SEQ ID No. 793;

25 SEQ ID No. 794; SEQ ID No. 808; SEQ ID No. 809; SEQ ID No. 838; SEQ ID No. 839; SEQ ID No. 840; SEQ ID No. 853; SEQ ID No. 854; SEQ ID No. 918; SEQ ID No. 923; SEQ ID No. 929; SEQ ID No. 931; SEQ ID No. 938; SEQ ID No. 939; SEQ ID No. 958; SEQ ID No. 959; SEQ ID No. 960; SEQ ID No. 966; SEQ ID No. 995; SEQ ID No. 1021; SEQ ID No. 1040; SEQ ID No. 1041; SEQ ID No. 1042; SEQ ID No. 1085; SEQ ID No. 1100; SEQ ID No. 1102; SEQ ID

30 No. 1117; SEQ ID No. 1118; SEQ ID No. 1119; SEQ ID No. 1120; SEQ ID No. 1135 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the intermediate metabolism of nucleotides or nucleic acids, and in that it is

35 chosen from the polypeptides having the following sequences:

SEQ ID No. 77; SEQ ID No. 78; SEQ ID No. 138; SEQ ID No. 189; SEQ ID No. 190; SEQ ID No. 233; SEQ ID No. 246; SEQ ID No. 338; SEQ ID No. 412; SEQ ID No. 421; SEQ ID No. 438;

SEQ ID No. 607; SEQ ID No. 648; SEQ ID No. 657; SEQ ID No. 740; SEQ ID No. 783; SEQ ID No. 967; SEQ ID No. 989; SEQ ID No. 990; SEQ ID No. 992; SEQ ID No. 1011; SEQ ID No. 1058; SEQ ID No. 1059; SEQ ID No. 1073; SEQ ID No. 1074 and one of their representative fragments.

5   Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of nucleic acids, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 14; SEQ ID No. 59; SEQ ID No. 70; SEQ ID No. 71; SEQ ID No. 97; SEQ ID
10   No. 113; SEQ ID No. 137; SEQ ID No. 141; SEQ ID No. 169; SEQ ID No. 285; SEQ ID No. 287; SEQ ID No. 288; SEQ ID No. 313; SEQ ID No. 326; SEQ ID No. 358; SEQ ID No. 411; SEQ ID No. 443; SEQ ID No. 548; SEQ ID No. 569; SEQ ID No. 601; SEQ ID No. 651; SEQ ID No. 654; SEQ ID No. 658; SEQ ID No. 659; SEQ ID No. 664; SEQ ID No. 665; SEQ ID No. 694; SEQ ID No. 698; SEQ ID No. 704; SEQ ID No. 760; SEQ ID No. 762; SEQ ID No. 763; SEQ ID No. 786;
15   SEQ ID No. 787; SEQ ID No. 788; SEQ ID No. 801; SEQ ID No. 802; SEQ ID No. 812; SEQ ID No. 819; SEQ ID No. 822; SEQ ID No. 870; SEQ ID No. 897; SEQ ID No. 898; SEQ ID No. 902; SEQ ID No. 908; SEQ ID No. 916; SEQ ID No. 954; SEQ ID No. 955; SEQ ID No. 961; SEQ ID No. 983; SEQ ID No. 996; SEQ ID No. 1007; SEQ ID No. 1012; SEQ ID No. 1013; SEQ ID No. 1014; SEQ ID No. 1015; SEQ ID No. 1038; SEQ ID No. 1137 and one of their representative
20   fragments.

          Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of amino acids or polypeptides, and in that it is chosen from the polypeptides having the following sequences:

25   SEQ ID No. 99; SEQ ID No. 111; SEQ ID No. 127; SEQ ID No. 134; SEQ ID No. 140; SEQ ID No. 174; SEQ ID No. 175; SEQ ID No. 176; SEQ ID No. 353; SEQ ID No. 377; SEQ ID No. 404; SEQ ID No. 523; SEQ ID No. 539; SEQ ID No. 559; SEQ ID No. 561; SEQ ID No. 586; SEQ ID No. 598; SEQ ID No. 609; SEQ ID No. 636; SEQ ID No. 687; SEQ ID No. 700; SEQ ID No. 701; SEQ ID No. 759; SEQ ID No. 790; SEQ ID No. 857; SEQ ID No. 861; SEQ ID No. 904; SEQ ID
30   No. 936; SEQ ID No. 952; SEQ ID No. 962; SEQ ID No. 963; SEQ ID No. 964; SEQ ID No. 965; SEQ ID No. 991; SEQ ID No. 1003; SEQ ID No. 1004; SEQ ID No. 1005; SEQ ID No. 1018; SEQ ID No. 1067; SEQ ID No. 1110; SEQ ID No. 1111; SEQ ID No. 1112; SEQ ID No. 1114; SEQ ID No. 1121; SEQ ID No. 1122; SEQ ID No. 1123; SEQ ID No. 1124; SEQ ID No. 1125 and one of their representative fragments.

35   Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of polypeptides, and in that it is chosen from the polypeptides

having the following sequences:

SEQ ID No. 4; SEQ ID No. 44; SEQ ID No. 45; SEQ ID No. 48; SEQ ID No. 54; SEQ ID No. 112; SEQ ID No. 130; SEQ ID No. 155; SEQ ID No. 163; SEQ ID No. 212; SEQ ID No. 257; SEQ ID No. 307; SEQ ID No. 343; SEQ ID No. 405; SEQ ID No. 416; SEQ ID No. 458; SEQ ID No. 540; SEQ ID No. 541; SEQ ID No. 542; SEQ ID No. 543; SEQ ID No. 544; SEQ ID No. 560; SEQ ID No. 594; SEQ ID No. 652; SEQ ID No. 699; SEQ ID No. 723; SEQ ID No. 747; SEQ ID No. 817; SEQ ID No. 827; SEQ ID No. 871; SEQ ID No. 909; SEQ ID No. 910; SEQ ID No. 911; SEQ ID No. 912; SEQ ID No. 1023; SEQ ID No. 1051; SEQ ID No. 1052; SEQ ID No. 1081 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of fatty acids, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 76; SEQ ID No. 284; SEQ ID No. 308; SEQ ID No. 309; SEQ ID No. 310; SEQ ID No. 311; SEQ ID No. 312; SEQ ID No. 425; SEQ ID No. 433; SEQ ID No. 565; SEQ ID No. 688; SEQ ID No. 690; SEQ ID No. 691; SEQ ID No. 767; SEQ ID No. 797; SEQ ID No. 894; SEQ ID No. 895; SEQ ID No. 994; SEQ ID No. 1020; SEQ ID No. 1030; SEQ ID No. 1033; SEQ ID No. 1034; SEQ ID No. 1046; SEQ ID No. 1047; SEQ ID No. 1057 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the synthesis of the wall, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 49; SEQ ID No. 50; SEQ ID No. 177; SEQ ID No. 178; SEQ ID No. 245; SEQ ID No. 610; SEQ ID No. 972; SEQ ID No. 974; SEQ ID No. 978; SEQ ID No. 1037 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the transcription, translation and/or maturation process, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 90; SEQ ID No. 92; SEQ ID No. 131; SEQ ID No. 151; SEQ ID No. 199; SEQ ID No. 333; SEQ ID No. 334; SEQ ID No. 336; SEQ ID No. 379; SEQ ID No. 589; SEQ ID No. 590; SEQ ID No. 619; SEQ ID No. 630; SEQ ID No. 649; SEQ ID No. 739; SEQ ID No. 741; SEQ ID No. 806; SEQ ID No. 821; SEQ ID No. 843; SEQ ID No. 968; SEQ ID No. 971; SEQ ID No. 1061 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* ribosomal polypeptide or one of its representative

fragments, and in that it is chosen from the polypeptides having the following sequences:
SEQ ID No. 93; SEQ ID No. 94; SEQ ID No. 95; SEQ ID No. 136; SEQ ID No. 259; SEQ ID
No. 332; SEQ ID No. 348; SEQ ID No. 583; SEQ ID No. 584; SEQ ID No. 588; SEQ ID No. 591;
SEQ ID No. 592; SEQ ID No. 663; SEQ ID No. 666; SEQ ID No. 667; SEQ ID No. 669; SEQ ID
5   No. 670; SEQ ID No. 671; SEQ ID No. 672; SEQ ID No. 673; SEQ ID No. 674; SEQ ID No. 675;
SEQ ID No. 676; SEQ ID No. 677; SEQ ID No. 678; SEQ ID No. 679; SEQ ID No. 680; SEQ ID
No. 681; SEQ ID No. 683; SEQ ID No. 684; SEQ ID No. 738; SEQ ID No. 781; SEQ ID No. 1008;
SEQ ID No. 1024; SEQ ID No. 1025; SEQ ID No. 1066 and one of their representative fragments.

Preferably, the invention also relates to a polypeptide according to the invention,
10 characterized in that it is a *Chlamydia pneumoniae* transport polypeptide or one of its representative
fragments, and in that it is chosen from the polypeptides having the following sequences:
SEQ ID No. 40; SEQ ID No. 41; SEQ ID No. 52; SEQ ID No. 105; SEQ ID No. 106; SEQ ID
No. 107; SEQ ID No. 109; SEQ ID No. 133; SEQ ID No. 210; SEQ ID No. 211; SEQ ID No. 214;
SEQ ID No. 215; SEQ ID No. 216; SEQ ID No. 217; SEQ ID No. 218; SEQ ID No. 219; SEQ ID
15 No. 220; SEQ ID No. 223; SEQ ID No. 242; SEQ ID No. 260; SEQ ID No. 293; SEQ ID No. 299;
SEQ ID No. 366; SEQ ID No. 369; SEQ ID No. 575; SEQ ID No. 602; SEQ ID No. 638; SEQ ID
No. 639; SEQ ID No. 640; SEQ ID No. 643; SEQ ID No. 653; SEQ ID No. 702; SEQ ID No. 703;
SEQ ID No. 724; SEQ ID No. 732; SEQ ID No. 855; SEQ ID No. 856; SEQ ID No. 901; SEQ ID
No. 906; SEQ ID No. 933; SEQ ID No. 942; SEQ ID No. 1043; SEQ ID No. 1086; SEQ ID
20 No. 1105 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention,
characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments
which is involved in the virulence process, and in that it is chosen from the polypeptides having the
following sequences:
25 SEQ ID No. 546; SEQ ID No. 550; SEQ ID No. 778; SEQ ID No. 779; SEQ ID No. 886 and one
of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention,
characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments
which is involved in the secretory system and/or which is secreted, and in that it is chosen from the
30 polypeptides having the following sequences:
SEQ ID No. 751; SEQ ID No. 874; SEQ ID No. 875; SEQ ID No. 876; SEQ ID No. 883; SEQ ID
No. 884; SEQ ID No. 885 and one of their representative fragments.

The secreted polypeptides, including the Type III and other, non-Type III secreted
polypeptides, of the present invention, as well as the corresponding nucleotide sequences, may be
35 detected by techniques known to persons skilled in the art, such as for example the techniques using
cloning combined with vectors allowing the expression of the said polypeptides fused to export
markers such as the *luc* gene for luciferase or the *PhoA* gene for alkaline phosphatase.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a polypeptide specific to *Chlamydia pneumoniae* or one of its representative fragments(with a Blast E value of $>10^{-5}$), and in that it is chosen from the polypeptides having the following sequences:

5   SEQ ID No. 7; SEQ ID No. 8; SEQ ID No. 17; SEQ ID No. 18; SEQ ID No. 19; SEQ ID No. 20; SEQ ID No. 22; SEQ ID No. 23; SEQ ID No. 24; SEQ ID No. 51; SEQ ID No. 60; SEQ ID No. 63; SEQ ID No. 65; SEQ ID No. 66; SEQ ID No. 67; SEQ ID No. 83; SEQ ID No. 84; SEQ ID No. 86; SEQ ID No. 87; SEQ ID No. 125; SEQ ID No. 143; SEQ ID No. 144; SEQ ID No. 179; SEQ ID No. 182; SEQ ID No. 184; SEQ ID No. 185; SEQ ID No. 187; SEQ ID No. 221;

10 SEQ ID No. 252; SEQ ID No. 254;; SEQ ID No. 278; SEQ ID No. 279; SEQ ID No. 387; SEQ ID No. 388; SEQ ID No. 397; SEQ ID No. 1048; SEQ ID No. 1049; SEQ ID No. 1050; SEQ ID No. 1128; SEQ ID No. 1130; SEQ ID No. 1131 and one of their representative fragments.

In general, in the present invention, the functional group to which a polypeptide of the invention belongs, as well as its corresponding nucleotide sequence, may be determined either by

15 comparative analogy with sequences already known, or by the use of standard techniques of biochemistry, of cytology combined with the techniques of genetic engineering such as immunoaffinity, localization by immunolabelling, differential extraction, measurement of enzymatic activity, study of the activity inducing or repressing expression or the study of expression in *E. coli*.

It is clearly understood, on the one hand, that, in the present invention, the nucleotide

20 sequences (ORF) and the amino acid sequences (SEQ ID No. 2 to SEQ ID No. 1291 and SEQ ID No. 6844 to SEQ ID No. 6848) which are listed by functional group, are not exhaustive within the group considered. Moreover, it is also clearly understood that, in the present invention, a nucleotide sequence (ORF) or an amino acid sequence mentioned within a given functional group may also be part of another group taking into account, for example, the interrelationship between the groups listed.

25 Accordingly, and as an example of this interrelationship, an exported and/or secreted polypeptide as well as its coding nucleotide sequence may also be involved in the *Chlamydia pneumoniae* virulence process by modifying the defense mechanism of the infected host cell, or a transmembrane polypeptide or its coding nucleotide sequence is also part of the polypeptides or coding nucleotide sequences of the cellular envelope.

30 The subject of the present invention is also the nucleotide and/or polypeptide sequences according to the invention, characterized in that the said sequences are recorded on a medium, called recording medium, whose type and nature facilitate the reading, the analysis and the exploitation of the said sequences. These media may of course also contain other information extracted from the present invention, such as in particular the analogies with already known sequences, such as those

35 mentioned in Table 1 of the present description, and/or may contain, in addition, information relating to the nucleotide and/or polypeptide sequences of other microorganisms so as to facilitate the comparative analysis and the exploitation of the results obtained.

Among these recording media, computer-readable media, such as magnetic, optical, electrical and hybrid media such as, for example, floppy disks, CD-ROMs or recording cassettes, are preferred in particular.

The invention also relates to nucleotide sequences which can be used as primer or probe, 5 characterized in that the said sequences are chosen from the nucleotide sequences according to the invention.

The invention relates, in addition, to the use of a nucleotide sequence according to the invention, as primer or probe, for the detection and/or amplification of nucleic acid sequences.

The nucleotide sequences according to the invention may thus be used to amplify 10 nucleotide sequences, in particular by the PCR technique (polymerase chain reaction) (Erlich, 1989; Innis et al., 1990; Rolfs et al., 1991, and White et al., 1997).

These oligodeoxyribonucleotide or oligoribonucleotide primers correspond to representative nucleotide fragments, and are advantageously at least 8 nucleotides, preferably at least 12 nucleotides, 15 nucleotides and still more preferably at least 20 nucleotides long.

15   Other techniques for amplifying the target nucleic acid may be advantageously used as alternatives to PCR.

The nucleotide sequences of the invention, in particular the primers according to the invention, may also be used in other methods for amplifying a target nucleic acid, such as:

- the TAS (Transcription-based Amplification System) technique described by Kwoh et al. in 1989;
20 - the 3SR (Self-Sustained Sequence Replication) technique described by Guatelli et al. in 1990;
- the NASBA (Nucleic Acid Sequence Based Amplification) technique described by Kievitis et al. in 1991;
- the SDA (Strand Displacement Amplification) technique (Walker et al., 1992);
- the TMA (Transcription Mediated Amplification) technique.

25   The polynucleotides of the invention may also be used in techniques for amplifying or for modifying the nucleic acid serving as probe, such as:

- the LCR (Ligase Chain Reaction) technique described by Landegren et al. in 1988 and perfected by Barany et al. in 1991, which uses a thermostable ligase;
- the RCR (Repair Chain Reaction) technique described by Segev in 1992;
30 - the CPR (Cycling Probe Reaction) technique described by Duck et al. in 1990;
- the Q-beta-replicase amplification technique described by Miele et al. in 1983 and perfected in particular by Chu et al. in 1986, Lizardi et al. in 1988, and then by Burg et al. as well as by Stone et al. in 1996.

The invention also relates to the nucleotide sequences of fragments which can be 35 obtained by amplification with the aid of at least one primer according to the invention. The present invention encompasses both hybridization probes and primers. In general, the complementary probes should be of a length sufficient to form a stable hybrid complex with the target sequences . Primers,

while complementary to the target sequences need not form stable hybridization complexes with the target sequences alone. Rather, primers form stable complexes with the target sequences in the presence of polymerase to permit extension of the primer.

In the case where the target polynucleotide to be detected is possibly an RNA, for example an mRNA, it will be possible to use, prior to the use of an amplification reaction with the aid of at least one primer according to the invention or to the use of a method of detection with the aid of at least one probe of the invention, a reverse transcriptase-type enzyme so as to obtain a cDNA from the RNA contained in the biological sample. The cDNA obtained will then serve as target for the primer(s) or the probe(s) used in the amplification or detection method according to the invention.

The detection probe will be chosen so that it hybridizes with the target sequence or the amplicon generated from the target sequence. Such a detection probe will advantageously have as sequence a sequence of at least 12 nucleotides, in particular of at least 20 nucleotides, and preferably at least 100 nucleotides.

The invention also comprises the nucleotide sequences which can be used as probe or primer according to the invention, characterized in that they are labelled with a radioactive compound or with a nonradioactive compound.

The nonlabelled nucleotide sequences may be used directly as probes or primers; however, the sequences are generally labelled with a radioactive element (^{32}P, ^{35}S, ^{3}H, ^{125}I) or with a nonradioactive molecule (biotin, acetylaminofluorene, digoxigenin, 5-bromo-deoxyuridine, fluorescein) so as to obtain probes which can be used in numerous applications.

Examples of nonradioactive labelling of nucleotide sequences are described, for example, in French patent No. 78,10975 or by Urdea et al. or by Sanchez-Pescador et al. in 1988.

In the latter case, one of the labelling methods described in patents FR-2 422 956 and FR-2 518 755 may also be used.

The invention also relates to the nucleotide sequences of fragments which can be obtained by hybridization with the aid of at least one probe according to the invention.

The hybridization technique may be performed in various ways (Matthews et al., 1988). The most common method consists in immobilizing the nucleic acid extracted from *Chlamydia pneumoniae* cells on a support (such as nitrocellulose, nylon, polystyrene) and in incubating, under well-defined conditions, the target nucleic acid immobilized with the probe. After hybridization, the excess probe is removed and the hybrid molecules formed are detected by the appropriate method (measurement of the radioactivity, of the fluorescence or of the enzymatic activity linked to the probe).

The invention also comprises the nucleotide sequences according to the invention, characterized in that they are covalently or noncovalently immobilized on a support.

According to another advantageous embodiment of the nucleic sequences according to the invention, the latter may be used immobilized on a support and may thus serve to capture, through

specific hybridization, the target nucleic acid obtained from the biological sample to be tested. If necessary, the solid support is separated from the sample and the hybridization complex formed between the so-called capture probe and the target nucleic acid is then detected by means of a second probe, called detection probe, labelled with an easily detectable element.

5   The nucleotide sequences according to the invention may also be used in new analytical systems, DNA chips, which allow sequencing, the study of mutations and of the expression of genes, and which are currently of interest given their very small size and their high capacity in terms of number of analyses.

             The principle of the operation of these chips is based on molecular probes, most often

10   oligonucleotides, which are attached onto a miniaturized surface, generally of the order of a few square centimetres. During an analysis, a sample containing fragments of a target nucleic acid to be analysed, for example DNA or RNA labelled, for example, after amplification, is deposited onto the DNA chip in which the support has been coated beforehand with probes. Bringing the labelled target sequences into contact with the probes leads to the formation, through hybridization, of a duplex

15   according to the rule of pairing defined by J.D. Watson and F. Crick. After a washing step, analysis of the surface of the chip allows the effective hybridizations to be located by means of the signals emitted by the labels tagging the target. A hybridization fingerprint results from this analysis which, by appropriate computer processing, will make it possible to determine information such as the presence of specific fragments in the sample, the determination of sequences and the presence of mutations.

20   The chip consists of a multitude of molecular probes, precisely organized or arrayed on a solid support whose surface is miniaturized. It is at the centre of a system where other elements (imaging system, microcomputer) allow the acquisition and interpretation of a hybridization fingerprint.

             The hybridization supports are provided in the form of flat or porous surfaces (pierced

25   with wells) composed of various materials. The choice of a support is determined by its physicochemical properties, or more precisely, by the relationship between the latter and the conditions under which the support will be placed during the synthesis or the attachment of the probes or during the use of the chip. It is therefore necessary, before considering the use of a particular support (R.S. Matson et al., 1994), to consider characteristics such as its stability to pH, its physical

30   strength, its reactivity and its chemical stability as well as its capacity to nonspecifically bind nucleic acids. Materials such as glass, silicon and polymers are commonly used. Their surface is, in a first step, called "functionalization", made reactive towards the groups which it is desired to attach thereon. After the functionalization, so-called spacer molecules are grafted onto the activated surface. Used as intermediates between the surface and the probe, these molecules of variable size render unimportant

35   the surface properties of the supports, which often prove to be problematic for the synthesis or the attachment of the probes and for the hybridization.

             Among the hybridization supports, there may be mentioned glass which is used, for

example, in the method of in situ synthesis of oligonucleotides by photochemical addressing developed by the company Affymetrix (E.L. Sheldon, 1993), the glass surface being activated by silane. Genosensor Consortium (P. Mérel, 1994) also uses glass slides carrying wells 3 mm apart, this support being activated with epoxysilane.

5   Polymers or silicon may also be mentioned among these hybridization supports. For example, the Andrein Mirzabekov team has developed a chip consisting of polyacrylamide squares polymerized on a silanized glass surface (G. Yershov et al., 1996). Several teams use silicon, in particular the IFOS laboratory of Ecole Centrale of Lyon which uses a silicon semiconductor substrate which is p-doped by introducing it into its crystalline structure atoms whose valency is different from
10   that of silicon. Various types of metals, in particular gold and platinum, may also be used as support (Genosensor Consortium (K. Beattie et al., 1993)).

          The probes according to the invention may be synthesized directly in situ on the supports of the DNA chips. This in situ synthesis may be carried out by photochemical addressing (developed by the company Affymax (Amsterdam, Holland) and exploited industrially by its subsidiary
15   Affymetrix (United States)) or based on the VLSIPS (very large scale immobilized polymer synthesis) technology (S.P.A. Fodor et al., 1991) which is based on a method of photochemically directed combinatory synthesis and the principle of which combines solid-phase chemistry, the use of photolabile protecting groups and photolithography.

          The probes according to the invention may be attached to the DNA chips in various ways
20   such as electrochemical addressing, automated addressing or the use of probe printers (T. Livache et al., 1994; G. Yershov et al., 1996; J. Derisi et al., 1996, and S. Borman, 1996).

          The revealing of the hybridization between the probes of the invention, deposited or synthesized in situ on the supports of the DNA chips, and the sample to be analysed, may be determined, for example, by measurement of fluorescent signals, by radioactive counting or by
25   electronic detection.

          The use of fluorescent molecules such as fluorescein constitutes the most common method of labelling the samples. It allows direct or indirect revealing of the hybridization and allows the use of various fluorochromes.

          Affymetrix currently provides an apparatus or a scanner designed to read its Gene Chip™
30   chips. It makes it possible to detect the hybridizations by scanning the surface of the chip in confocal microscopy (R.J. Lipshutz et al., 1995). Other methods of detecting fluorescent signals have been tested: coupling of an epifluorescence microscope and a CCD camera (G. Yershov et al., 1996), the use of an optical fibre collecting system (E.L. Sheldon, 1993). A conventional method consists in carrying out an end labelling, with phosphorus 32, of the target sequences, by means of an appropriate
35   apparatus, the Phosphorimager (marketed by Molecular Dynamics). The electronic detection is based on the principle that the hybridization of two nucleic acid molecules is accompanied by physical phenomena which can be quantified under certain conditions (system developed by Ecole Centrale of

Lyon and called GEN-FET (GEN field effect transistor)). Genosensor Consortium and the company Beckman Instruments who are developing an electronic chip or Permittivity Chips™ may also be mentioned (K. Beattie et al., 1993).

5   The nucleotide sequences according to the invention may thus be used in DNA chips to carry out the analysis of mutations. This analysis is based on the production of chips capable of analysing each base of a nucleotide sequence according to the invention.

        The nucleotide sequences according to the invention may also be used in DNA chips to carry out the analysis of the expression of the *Chlamydia pneumoniae* genes. This analysis of the expression of *Chlamydia pneumoniae* genes is based on the use of chips where probes of the
10   invention, chosen for their specificity to characterize a given gene, are present (D.J. Lockhart et al., 1996; D.D. Shoemaker et al., 1996). For the methods of analysis of gene expression using the DNA chips, reference may, for example, be made to the methods described by D.J. Lockhart et al. (1996) and Sosnowsky et al. (1997) for the synthesis of probes in situ or for the addressing and the attachment of previously synthesized probes. The target sequences to be analysed are labelled and in general
15   fragmented into sequences of about 50 to 100 nucleotides before being hybridized onto the chip. After washing as described, for example, by D.J. Lockhart et al. (1996) and application of different electric fields (Sosnowsky et al., 1997), the labelled compounds are detected and quantified, the hybridizations being carried out at least in duplicate. Comparative analyses of the signal intensities obtained with respect to the same probe for different samples and/or for different probes with the same sample,
20   determine the differential expression of RNA or of DNA derived from the sample.

        The nucleotide sequences according to the invention may, in addition, be used in DNA chips where other nucleotide probes specific for other microorganisms are also present, and may allow the carrying out of a serial test allowing rapid identification of the presence of a microorganism in a sample.

25   Accordingly, the subject of the invention is also the nucleotide sequences according to the invention, characterized in that they are immobilized on a support of a DNA chip.

        The DNA chips, characterized in that they contain at least one nucleotide sequence according to the invention, immobilized on the support of the said chip, also form part of the invention.

30   The said chips will preferably contain several probes or nucleotide sequences of the invention of different length and/or corresponding to different genes so as to identify, with greater certainty, the specificity of the target sequences or the desired mutation in the sample to be analysed.

        Accordingly, the analyses carried out by means of primers and/or probes according to the invention, immobilized on supports such as DNA chips, will make it possible, for example, to identify,
35   in samples, mutations linked to variations such as intraspecies variations. These variations may be correlated or associated with pathologies specific to the variant identified and will make it possible to select the appropriate treatment.

The invention thus comprises a DNA chip according to the invention, characterized in that it contains, in addition, at least one nucleotide sequence of a microorganism different from *Chlamydia pneumoniae,* immobilized on the support of the said chip; preferably, the different microorganism will be chosen from an associated microorganism, a bacterium of the

5   *Chlamydia* family, and a variant of the species *Chlamydia pneumoniae.*

Another subject of the present invention is a vector for the cloning and/or the expression of a sequence, characterized in that it contains a nucleotide sequence according to the invention. Among the said vectors according to the invention, the vectors containing a nucleotide sequence encoding a polypeptide of the cellular, preferably outer, envelope of *Chlamydia pneumoniae* or one of

10 its representative fragments, are preferred. In a specific embodiment, the vectors contain a nucleotide sequence encoding a *Chlamydia pneumoniae* secreted polypeptide or one of its representative fragments or encoding a transport polypeptide, a surface exposed polypeptide, a lipoprotein or one of its representative fragments, a polypeptide involved in lipopolysaccharide (LPS) biosynthesis, a Type III and non-Type III secreted polypeptide, a polypeptide containing RGD attachment sites, a cell wall

15 anchored surface polypeptide, a polypeptide not found in *Chlamydia trachomatis,* a ribosomal polypeptide or a polypeptide involved in secretion, transcription, translation, maturation of proteins, a polypeptide involved in the synthesis of the wall, a polypeptide involved in the virulence, a polypeptide involved in the intermediate metabolism, in particular in the metabolism of sugars and/or of cofactors, a polypeptide involved in the metabolism of nucleotides, of amino acids, of nucleic acids

20 or of fatty acids of *Chlamydia pneumoniae* or one of their representative fragments, or a polypeptide specific to *Chlamydia pneumoniae.*

According to the invention, the vectors comprise the elements necessary to allow the expression and/or the secretion of the said nucleotide sequences in a given host cell, and form part of the invention. The vector should, in this case, comprise a promoter, signals for initiation and for

25 termination of translation, as well as appropriate regions for regulation of transcription. It should be capable of being stably maintained in the host cell and may optionally possess particular signals specifying the secretion of the translated protein. These different elements are chosen according to the host cell used. To this effect, the nucleotide sequences according to the invention may be inserted into autonomously-replicating vectors within the chosen host, or integrative vectors in the chosen host.

30 Any of the standard methods known to those skilled in the art for the insertion of DNA fragments into a vector may be used to construct expression vectors containing a chimeric gene consisting of appropriate transcriptional/translational control signals and the protein coding sequences. These methods may include *in vitro* recombinant DNA and synthetic techniques and *in vivo* recombinants (genetic recombination).

35 Expression of a polypeptide, peptide or derivative, or analogs thereof encoded by a polynucleotide sequence in SEQ ID No. 1 or ORFs contained within SEQ ID No. 1 may be regulated by a second nucleic acid sequence so that the protein or peptide is expressed in a host transformed

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with the recombinant DNA molecule. For example, expression of a protein or peptide may be controlled by any promoter/enhancer element known in the art. Promoters which may be used to control expression include, but are not limited to, the CMV promoter, the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto, et al., 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner et al., 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et al., 1982, Nature 296:39-42); prokaryotic expression vectors such as the Ǝ-lactamase promoter (Villa-Kamaroff, et al., 1978, Proc. Natl. Acad. Sci. U.S.A. 75:3727-3731), or the tac promoter (DeBoer, et al., 1983, Proc. Natl. Acad. Sci. U.S.A. 80:21-25); see also "Useful proteins from recombinant bacteria" in Scientific American, 1980, 242:74-94; plant expression vectors comprising the nopaline synthetase promoter region (Herrera-Estrella et al., 1983, Nature 303:209-213) or the cauliflower mosaic virus 35S RNA promoter (Gardner, et al., 1981, Nucl. Acids Res. 9:2871), and the promoter of the photosynthetic enzyme ribulose biphosphate carboxylase (Herrera-Estrella et al., 1984, Nature 310:115-120); promoter elements from yeast or other fungi such as the Gal 4 promoter, the ADC (alcohol dehydrogenase) promoter, PGK (phosphoglycerol kinase) promoter, alkaline phosphatase promoter, and the following animal transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: elastase I gene control region which is active in pancreatic acinar cells (Swift et al., 1984, Cell 38:639-646; Ornitz et al., 1986, Cold Spring Harbor Symp. Quant. Biol. 50:399-409; MacDonald, 1987, Hepatology 7:425-515); insulin gene control region which is active in pancreatic beta cells (Hanahan, 1985, Nature 315:115-122), immunoglobulin gene control region which is active in lymphoid cells (Grosschedl et al., 1984, Cell 38:647-658; Adames et al., 1985, Nature 318:533-538; Alexander et al., 1987, Mol. Cell. Biol. 7:1436-1444), mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and mast cells (Leder et al., 1986, Cell 45:485-495), albumin gene control region which is active in liver (Pinkert et al., 1987, Genes and Devel. 1:268-276), alpha-fetoprotein gene control region which is active in liver (Krumlauf et al., 1985, Mol. Cell. Biol. 5:1639-1648; Hammer et al., 1987, Science 235:53-58; alpha 1-antitrypsin gene control region which is active in the liver (Kelsey et al., 1987, Genes and Devel. 1:161-171), beta-globin gene control region which is active in myeloid cells (Mogram et al., 1985, Nature 315:338-340; Kollias et al., 1986, Cell 46:89-94; myelin basic protein gene control region which is active in oligodendrocyte cells in the brain (Readhead et al., 1987, Cell 48:703-712); myosin light chain-2 gene control region which is active in skeletal muscle (Sani, 1985, Nature 314:283-286), and gonadotropic releasing hormone gene control region which is active in the hypothalamus (Mason et al., 1986, Science 234:1372-1378).

The vectors according to the invention are, for example, vectors of plasmid or viral origin. In a specific embodiment, a vector is used that comprises a promoter operably linked to a protein or peptide-encoding a nucleic acid sequence in SEQ ID No. 1, or ORFs contained within SEQ ID No. 1, one or more origins of replication, and, optionally, one or more selectable markers (e.g., an

antibiotic resistance gene). Expression vectors comprise regulatory sequences that control gene expression, including gene expression in a desired host cell. Preferred vectors for the expression of the polypeptides of the invention include the pET-type plasmid vectors (Promega) or pBAD plasmid vectors (Invitrogen). Furthermore, the vectors according to the invention are useful for transforming

5   host cells so as to clone or express the nucleotide sequences of the invention.

Expression can also be achieved using targeted homologous recombination to activate *Chlamydia pneumoniae* genes present in the cloned genomic DNA. A heterologous regulatory element may be inserted into a stable cell line or cloned microorganism, such that it is operatively linked with an endogenous *Chlamydia pneumoniae* gene present in the cloned genome, using

10 techniques, such as targeted homologous recombination, which are well known to those of skill in the art (*See, e.g.,* Chappel, U.S. Patent No. 4,215,051 and Skoultchi, WO 91/06667 each of which is incorporated herein in its entirety).

Expression vector/host cell systems containing inserts of polynucleotide sequences in SEQ ID No. 1 or ORFs within SEQ ID No. 1, which encode polypeptides, peptides or derivatives, or

15 analogs thereof, can be identified by three general approaches: (a) nucleic acid hybridization, (b) presence or absence of "marker" gene functions, and (c) expression of inserted sequences. In the first approach, the presence of a polynucleotide sequence inserted in an expression vector can be detected by nucleic acid hybridization using probes comprising sequences that are homologous to an inserted polynucleotide sequence. In the second approach, the recombinant vector/host system can be

20 identified and selected based upon the presence or absence of certain "marker" gene functions (*e.g.,* thymidine kinase activity, resistance to antibiotics, transformation phenotype, occlusion body formation in baculovirus, etc.) caused by the insertion of a polynucleotide sequence in the vector. For example, if the polynucleotide sequence in SEQ ID No. 1 or ORFs within SEQ ID No. 1 is inserted within the marker gene sequence of the vector, recombinants containing the insert can be identified by

25 the absence of the marker gene function. In the third approach, recombinant expression vectors can be identified by assaying the product of the polynucleotide sequence expressed by the recombinant. Such assays can be based, for example, on the physical or functional properties of the expressed polypeptide in *in vitro* assay systems, *e.g.,* binding with antibody, promotion of cell proliferation.

Once a particular recombinant DNA molecule is identified and isolated, several methods

30 known in the art may be used to propagate it. The clones identified may be introduced into an appropriate host cell by standard methods, such as for example lipofection, electroporation, and heat shock. Once a suitable host system and growth conditions are established, recombinant expression vectors can be propagated and prepared in quantity.

The invention also encompasses the host cells transformed by a vector according to the

35 invention. These cells may be obtained by introducing into host cells a nucleotide sequence inserted into a vector as defined above, and then culturing the said cells under conditions allowing the replication and/or the expression of the transfected nucleotide sequence.

The host cell may be chosen from eukaryotic or prokaryotic systems, such as for example bacterial cells (Olins and Lee, 1993), but also yeast cells (Buckholz, 1993), as well as animal cells, in particular cultures of mammalian cells (Edwards and Aruffo, 1993), and in particular Chinese hamster ovary (CHO) cells, but also insect cells in which methods using baculoviruses for example
5 may be used (Luckow, 1993).

Furthermore, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Expression from certain promoters can be elevated in the presence of certain inducers; thus, expression of the genetically engineered polypeptide may be controlled. Furthermore, different host
10 cells have characteristic and specific mechanisms for the translational and post-translational processing and modification (e.g., glycosylation, phosphorylation) of proteins. Appropriate cell lines or host systems can be chosen to ensure the desired modification and processing of the foreign protein expressed. For example, expression in a bacterial system can be used to produce an unglycosylated core protein product. Expression in yeast will produce a glycosylated product. Expression in
15 mammalian cells can be used to ensure "native" glycosylation of a heterologous protein. Furthermore, different vector/host expression systems may effect processing reactions to different extents.

A preferred host cell for the expression of the proteins of the invention consists of prokaryotic cells, such as Gram bacteria. A further preferred host cell according to the invention is a bacterium belonging to the *Chlamydia* family, more preferably belonging to the species *Chlamydia*
20 *pneumoniae* or chosen from a microorganism associated with the species *Chlamydia pneumoniae*.

In other specific embodiments, the polypeptides, peptides or derivatives, or analogs thereof may be expressed as a fusion, or chimeric protein product (comprising the protein, fragment, analog, or derivative joined via a peptide bond to a heterologous protein sequence (of a different protein)). Such a chimeric product can be made by ligating the appropriate nucleic acid sequences
25 encoding the desired amino acid sequences to each other by methods known in the art, in the proper coding frame, and expressing the chimeric product by methods commonly known in the art. Alternatively, such a chimeric product may be made by protein synthetic techniques, e.g., by use of a peptide synthesizer.

Genomic sequences can be cloned and expressed as translational gene products (i.e.,
30 peptides, polypeptides, and proteins) or transcriptional gene products (i.e., antisense and ribozymes).

The invention further relates to the intracellular production of an antisense nucleic acid sequence of SEQ ID No. 1 by transcription from an exogenous sequence. For example, a vector can be introduced *in vivo* such that it is taken up by a cell, within which cell the vector or a portion thereof is transcribed, producing an antisense nucleic acid (RNA) of the invention. Such a vector would
35 contain a sequence encoding an antisense nucleic acid. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art.

Vectors can be plasmid, viral, or others known in the art, used for replication and expression in mammalian cells. Expression of the sequence encoding the an antisense RNA can be by any promoter known in the art to act in mammalian, preferably human, cells. Such promoters can be inducible or constitutive. Such promoters include but are not limited to: the CMV promoter, the SV40 early

5   promoter region (Bernoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 3N long terminal repeat of Rous sarcoma virus (Yamamoto *et al.*, 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner *et al.*, 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster *et al.*, 1982, Nature 296:39-42), etc.

In a specific embodiment, the antisense oligonucleotide comprises catalytic RNA, or a

10 ribozyme (see, *e.g.*, PCT International Publication WO 90/11364, published October 4, 1990; Sarver *et al.*, 1990, Science 247:1222-1225). In another embodiment, the oligonucleotide is a 2N-0-methylribonucleotide (Inoue *et al.*, 1987, Nucl. Acids Res. 15:6131-6148), or a chimeric RNA-DNA analog (Inoue *et al.*, 1987, FEBS Lett. 215:327-330).

In another embodiment, the antisense nucleic acids of the invention comprise a sequence

15 complementary to at least a portion of an RNA transcript of a polynucleotide sequence in SEQ ID No. 1. However, absolute complementarity, although preferred, is not required. A sequence "complementary to at least a portion of an RNA," as referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acid sequence, a single strand of the duplex DNA may thus be

20 tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA transcribed from SEQ ID No. 1 may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the

25 hybridized complex.

The invention also relates to the animals, except humans, comprising one of the above-described transformed cells according to the invention.

The production of transgenic animals according to the invention overexpressing one or more of the *Chlamydia pneumoniae* genes will be preferably carried out on rats, mice or rabbits

30 according to methods well known to persons skilled in the art such as viral or nonviral transfections. The transgenic animals overexpressing one or more of the said genes may be obtained by transfection of multiple copies of the said genes under the control of a powerful promoter of a ubiquitous nature, or which is selective for one type of tissue. The transgenic animals may also be obtained by homologous recombination on embryonic stem cells, transfer of these stem cells to embryos, selection of the

35 chimeras affected at the level of the reproductive lines, and growth of the said chimeras.

The transformed cells as well as the transgenic animals according to the invention can be used in methods of preparing the recombinant polypeptide.

It is now possible to produce recombinant polypeptides in a relatively large quantity by genetic engineering using the cells transformed with expression vectors according to the invention or using transgenic animals according to the invention.

The methods of preparing a polypeptide of the invention in recombinant form,
5 characterized in that they use a vector and/or a cell transformed with a vector according to the invention and/or a transgenic animal comprising one of the said transformed cells according to the invention, are themselves included in the present invention.

Among the said methods of preparing a polypeptide of the invention in recombinant form, the methods of preparation using a vector, and/or a cell transformed with the said vector and/or a
10 transgenic animal comprising one of the said transformed cells, containing a nucleotide sequence encoding a polypeptide of the cellular envelope of *Chlamydia pneumoniae* or one of its representative fragments, more preferably encoding a polypeptide of the outer cellular envelope of *Chlamydia pneumoniae* or one of its fragment, are preferred.

Among the said methods of preparing a polypeptide of the invention in recombinant
15 form, the methods of preparation using a vector, and/or a cell transformed with the said vector and/or a transgenic animal comprising one of the said transformed cells, containing a nucleotide sequence encoding a *Chlamydia pneumoniae* secreted polypeptide or one of its representative fragments or encoding a transport polypeptide, a surface exposed polypeptide, a lipoprotein or one of its representative fragments, a polypeptide involved in lipopolysaccharide biosynthesis, a Type III or
20 other secreted polypeptide, a polypeptide containing RGD attachment sites, a cell wall anchored surface polypeptide, a polypeptide not found in *Chlamydia trachomatis*, a ribosomal polypeptide or a polypeptide involved in secretion, transcription, translation, maturation of proteins, a polypeptide involved in the synthesis of the wall, a polypeptide involved in the virulence, a polypeptide involved in the intermediate metabolism, in particular in the metabolism of sugars and/or of cofactors, a
25 polypeptide involved in the metabolism of nucleotides, of amino acids, of nucleic acids or of fatty acids of *Chlamydia pneumoniae* or one of their representative fragments, or a polypeptide specific to *Chlamydia pneumoniae*, are also preferred.

The recombinant polypeptides obtained as indicated above may be provided either in glycosylated or non-glycosylated form and may or may not have the natural tertiary structure.
30 A preferred variant consists in producing a recombinant polypeptide fused to a "carrier" protein (chimeric protein). The advantage of this system is that it allows a stabilization and a reduction in proteolysis of the recombinant product, an increase in solubility during renaturation in vitro and/or a simplification of purification when the fusion partner has affinity for a specific ligand.

More particularly, the invention relates to a method of preparing a polypeptide of the
35 invention comprising the following steps:

a) culture of the transformed cells under conditions allowing the expression of a recombinant polypeptide having a nucleic acid sequence according to the invention;

b) where appropriate, recovery of the said recombinant polypeptide.

When the method of preparing a polypeptide of the invention uses a transgenic animal according to the invention, the recombinant polypeptide is then extracted from the said animal.

The subject of the invention is also a polypeptide capable of being obtained by a method of the invention as described above.

The invention also comprises a method of preparing a synthetic polypeptide, characterized in that it uses an amino acid sequence of polypeptides according to the invention.

The invention also relates to a synthetic polypeptide obtained by a method according to the invention.

Polypeptides according to the invention may also be prepared by conventional techniques in the field of peptide synthesis under conditions suitable to produce the polypeptides encoded by the polynucleotide of the invention. This synthesis may be carried out in and recovered from a homogeneous solution or on a solid phase.

For example, the synthesis technique in a homogeneous solution described by Houbenweyl in 1974 may be used.

This method of synthesis consists in successively condensing, in pairs, the successive amino acids in the required order, or in condensing amino acids and fragments previously formed and already containing several amino acids in the appropriate order, or alternatively several fragments thus previously prepared, it being understood that care will have been taken to protect beforehand all the reactive functional groups carried by these amino acids or fragments, with the exception of the amine functional groups of one and the carboxyl functional groups of the other or vice versa, which should normally take part in the formation of the peptide bonds, in particular after activation of the carboxyl functional group, according to methods well known in peptide synthesis.

According to another preferred technique of the invention, the one described by Merrifield is used.

To manufacture a peptide chain according to the Merrifield method, a highly porous polymer resin is used, onto which the first C-terminal amino acid of the chain is attached. This amino acid is attached onto a resin via its carboxyl group and its amine functional group is protected. The amino acids which will constitute the peptide chain are thus attached, one after another, onto the amine group, each time deprotected beforehand, of the portion of the peptide chain already formed, and which is attached to the resin. When the entire peptide chain desired is formed, the protecting groups are removed from the various amino acids constituting the peptide chain and the peptide is detached from the resin with the aid of an acid.

The invention relates, in addition, to hybrid (fusion) polypeptides having at least one polypeptide or one of its representative fragments according to the invention, and a sequence of a polypeptide capable of eliciting an immune response in humans or animals.

Advantageously, the antigenic determinant is such that it is capable of eliciting a humoral

and/or cellular response. An antigenic determinant may be identified by screening expression libraries of the *Chlamydia pneumoniae* genome with antibodies contained in the serum of patients infected with a bacterium belonging to the species *Chlamydia pneumoniae*. An antigenic determinant may comprise a polypeptide or one of its representative fragments according to the

5   invention, in glycosylated form, used in order to obtain immunogenic compositions capable of inducing the synthesis of antibodies directed against multiple epitopes. The said polypeptides or their glycosylated fragments also form part of the invention.

These hybrid molecules may consist, in part, of a carrier molecule for polypeptides or for their representative fragments according to the invention, combined with a portion which may be

10   immunogenic, in particular an epitope of the diphtheria toxin, the tetanus toxin, a hepatitis B virus surface antigen (patent FR 79 21811), the poliomyelitis virus VP1 antigen or any other viral or bacterial toxin or antigen.

The methods of synthesizing the hybrid molecules include the methods used in genetic engineering to construct hybrid nucleotide sequences encoding the desired polypeptide sequences.

15   Reference may be advantageously made, for example, to the technique for producing genes encoding fusion proteins described by Minton in 1984.

The said hybrid nucleotide sequences encoding a hybrid polypeptide as well as the hybrid polypeptides according to the invention, characterized in that they are recombinant polypeptides obtained by the expression of the said hybrid nucleotide sequences, also form part of the invention.

20   The invention also comprises the vectors characterized in that they contain one of the said hybrid nucleotide sequences. The host cells transformed by the said vectors, the transgenic animals comprising one of the said transformed cells as well as the methods of preparing recombinant polypeptides using the said vectors, the said transformed cells and/or the said transgenic animals of course also form part of the invention.

25   The polypeptides according to the invention, the antibodies according to the invention described below and the nucleotide sequences according to the invention may advantageously be used in *in vitro* and/or *in vivo* methods for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae*, in a biological sample (biological tissue or fluid) which is likely to contain them. These methods, depending on the specificity of the polypeptides, of the antibodies

30   and of the nucleotide sequences according to the invention which will be used, may in particular detect and/or identify the bacterial variants belonging to the species *Chlamydia pneumoniae* as well as the associated microorganisms capable of being detected by the polypeptides, the antibodies and the nucleotide sequences according to the invention which will be chosen. It may, for example, be advantageous to choose a polypeptide, an antibody or a nucleotide sequence according to the

35   invention, which is capable of detecting any bacterium of the Chlamydia family by choosing a polypeptide, an antibody and/or a nucleotide sequence according to the invention which is specific to the family or, on the contrary, it will be most particularly advantageous to target a variant of the

species *Chlamydia pneumoniae*, which is responsible, for example, for the induction or the worsening of pathologies specific to the targeted variant, by choosing a polypeptide, an antibody and/or a nucleotide sequence according to the invention which is specific to the said variant.

5   The polypeptides according to the invention may advantageously be used in a method for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, in a biological sample (biological tissue or fluid) which is likely to contain them, characterized in that it comprises the following steps:

a)   bringing this biological sample into contact with a polypeptide or one of its representative fragments according to the invention (under conditions allowing an immunological reaction between 10 the said polypeptide and the antibodies which may be present in the biological sample);

b)   detecting the antigen-antibody complexes which may be formed.

Preferably, the biological sample consists of a fluid, for example a human or animal serum, blood or biopsies.

Any conventional procedure may be used to carry out such a detection of the antigen- 15 antibody complexes which may be formed.

By way of example, a preferred method uses immunoenzymatic procedures based on the ELISA technique, immunofluorescence procedures or radioimmunological procedures (RIA), and the like.

Accordingly, the invention also relates to the polypeptides according to the invention, 20 labelled with the aid of a suitable label such as a label of the enzymatic, fluorescent or radioactive type.

Such methods comprise, for example, the following steps:

-      deposition of defined quantities of a polypeptide composition according to the invention into the wells of a microtitre plate,

25 -   introduction, into the said wells, of increasing dilutions of serum, or of a different biological sample as defined above, which has to be analysed,

-      incubation of the microplate,

-      introduction, into the wells of the microtitre plate, of labelled antibodies directed against human or animal immunoglobulins, these antibodies having been labelled with the aid of an enzyme 30   selected from those which are capable of hydrolyzing a substrate, thereby modifying the absorption of the radiation of the latter, at least at a defined wavelength, for example at 550 nm,

-      detection, by comparison with a control, of the quantity of substrate hydrolyzed.

The invention also relates to a kit or set for the detection and/or the identification of 35 bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, characterized in that it comprises the following components:

-      a polypeptide according to the invention,

- where appropriate, the reagents for constituting the medium appropriate for the immunological or specific reaction,

- the reagents allowing the detection of the antigen-antibody complexes produced by the immuno-logical reaction between the polypeptide(s) of the invention and the antibodies which may be

5   present in the biological sample, it being possible for these reagents also to carry a label, or to be capable of being recognized in turn by a labelled reagent, more particularly in the case where the polypeptide according to the invention is not labelled,

- where appropriate, a reference biological sample (negative control) free of antibodies recognized by a polypeptide according to the invention,

10 - where appropriate, a reference biological sample (positive control) containing a predetermined quantity of antibodies recognized by a polypeptide according to the invention.

According to the invention, the polypeptides, peptides, fusion proteins or other derivatives, or analogs thereof encoded by a polynucleotide sequence in SEQ ID No. 1, may be used as an immunogen to generate antibodies which immunospecifically bind such an immunogen. Such

15 antibodies may include, but are not limited to, polyclonal and monoclonal antibodies, humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab')$_2$ fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies, and epitope-binding fragments of any of the above. In a specific embodiment, the antibody to a polypeptide, peptide or other derivative, or analog thereof encoded by a polynucleotide sequence in SEQ ID No. 1 is a bispecific antibody (see

20 generally, e.g. Fanger and Drakeman, 1995, Drug News and Perspectives 8: 133-137). Such a bispecific antibody is genetically engineered to recognize both (1) an epitope and (2) one of a variety of "trigger" molecules, e.g. Fc receptors on myeloid cells, and CD3 and CD2 on T cells, that have been identified as being able to cause a cytotoxic T-cell to destroy a particular target. Such bispecific antibodies can be prepared either by chemical conjugation, hybridoma, or recombinant molecular

25 biology techniques known to the skilled artisan.

Various procedures known in the art may be used for the production of polyclonal antibodies to a polypeptide, peptide or other derivative, or analog thereof encoded by a polynucleotide sequence in SEQ ID No. 1. For the production of antibody, various host animals can be immunized by injection with a polypeptide, or peptide or other derivative, or analog thereof, including but not limited

30 to rabbits, mice, rats, etc. Various adjuvants, depending on the host species, may be used to increase the immunological response, including but not limited to Stimulon™ QS-21 (Aquila Biopharmaceuticals, Inc., Framingham, MA), MPL™ (3-O-deacylated monophosphoryl lipid A; RIBI ImmunoChem Research, Inc., Hamilton, MT), aluminum phosphate, IL-12 (Genetics Institute, Cambridge, MA), Freund's (complete and incomplete), mineral gels such as aluminum hydroxide,

35 surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, BCG (bacille Calmette-Guerin), and corynebacterium parvum. Alternatively, polyclonal antibodies may be prepared by purifying, on an affinity column

onto which a polypeptide according to the invention has been previously attached, the antibodies contained in the serum of patients infected with a bacterium belonging to the species *Chlamydia pneumoniae*.

For preparation of monoclonal antibodies directed toward a polypeptide, peptide or other derivative, or analog, any technique which provides for the production of antibody molecules by continuous cell lines in culture may be used. For example, the hybridoma technique originally developed by Kohler and Milstein (1975, Nature 256:495-497), as well as the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, 1983, Immunology Today 4:72), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole *et al.*, 1985, in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc., pp. 77-96). In an additional embodiment of the invention, monoclonal antibodies can be produced in germ-free animals utilizing technology described in PCT/US90/02545. In another embodiment of the invention, transgenic non-human animals can be used for the production of human antibodies utilizing technology described in WO 98/24893 and WO 96/33735. According to the invention, human antibodies may be used and can be obtained by using human hybridomas (Cote *et al.*, 1983, Proc. Natl. Acad. Sci. U.S.A. 80:2026-2030) or by transforming human B cells with EBV virus *in vitro* (Cole *et al.*, 1985, in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, pp. 77-96). In fact, according to the invention, techniques developed for the production of "chimeric antibodies" (Morrison *et al.*, 1984, PROC. NATL. ACAD. SCI. U.S.A. 81:6851-6855; Neuberger *et al.*, 1984, Nature 312:604-608; Takeda *et al.*, 1985, Nature 314:452-454) by splicing the genes from a mouse antibody molecule specific for a polypeptide, peptide or other derivative, or analog together with genes from a human antibody molecule of appropriate biological activity can be used; such antibodies are within the scope of this invention.

According to the invention, techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce polypeptide or peptide-specific single chain antibodies. An additional embodiment of the invention utilizes the techniques described for the construction of Fab expression libraries (Huse *et al.*, 1989, Science 246:1275-1281) to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity for polypeptides, derivatives, or analogs.

Antibody fragments which contain the idiotype of the molecule can be generated by known techniques. For example, such fragments include but are not limited to: the F(ab')$_2$ fragment which can be produced by pepsin digestion of the antibody molecule; the Fab' fragments which can be generated by reducing the disulfide bridges of the F(ab')$_2$ fragment, the Fab fragments which can be generated by treating the antibody molecule with papain and a reducing agent, and Fv fragments.

In addition, techniques have been developed for the production of chimerized (*See, e.g.*, Boss, M. et al., U.S. Patent No. 4,816,397; and Cabilly, S. et al., U.S. Patent No. 5,585,089 each of which is incorporated herein by reference in its entirety) humanized antibodies (*See, e.g.*, Queen, U.S. Patent No. 5,585,089, which is incorporated herein by reference in its entirety.) An immunoglobulin

light or heavy chain variable region consists of a "framework" region interrupted by three hypervariable regions, referred to as complementarily determining regions (CDRs). The extent of the framework region and CDRs have been precisely defined (See, "Sequences of Proteins of Immunological Interest", Kabat, E. et al., U.S. Department of Health and Human Services (1983).

5   Briefly, humanized antibodies are antibody molecules from non-human species having one or more CDRs from the non-human species and a framework from a human immunoglobulin molecule.

The antibodies of the invention may also be labelled in the same manner as described above for the nucleic probes of the invention such as an enzymatic, fluorescent or radioactive type labelling.

10   The invention relates, in addition, to a method for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism in a biological sample, characterized in that it comprises the following steps:

a)   bringing the biological sample (biological tissue or fluid) into contact with a mono- or polyclonal antibody according to the invention (under conditions allowing an immunological reaction

15   ·   between the said antibodies and the polypeptides of the bacterium belonging to the species *Chlamydia pneumoniae* or to an associated microorganism which may be present in the biological sample, that is, under conditions suitable for the formation of immune complexes);

b)   detecting the antigen-antibody complex which may be formed.

20   Also falling within the scope of the invention is a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, characterized in that it comprises the following components:

-    a polyclonal or monoclonal antibody according to the invention, labeled where appropriate;

-    where appropriate, a reagent for constituting the medium appropriate for carrying out the

25   immunological reaction;

-    a reagent allowing the detection of the antigen-antibody complexes produced by the immunological reaction, it being possible for this reagent also to carry a label, or to be capable of being recognized in turn by a labelled reagent, more particularly in the case where the said monoclonal or polyclonal antibody is not labelled;

30   -   where appropriate, reagents for carrying out the lysis of the cells in the sample tested.

The principle of the DNA chip which was explained above may also be used to produce protein "chips" on which the support has been coated with a polypeptide or an antibody according to the invention, or arrays thereof, in place of the DNA. These protein "chips" make it possible, for example, to analyze the biomolecular interactions (BIA) induced by the affinity capture of target

35   analytes onto a support coated, for example, with proteins, by surface plasma resonance (SPR). Reference may be made, for example, to the techniques for coupling proteins onto a solid support which are described in EP 524 800 or to the methods describing the use of biosensor-type protein

chips such as the BIAcore-type technique (Pharmacia) (Arlinghaus et al., 1997, Krone et al., 1997, Chatelier et al., 1995). These polypeptides or antibodies according to the invention, capable of specifically binding antibodies or polypeptides derived from the sample to be analysed, may thus be used in protein chips for the detection and/or the identification of proteins in samples. The said protein

5 chips may in particular be used for infectious diagnosis and may preferably contain, per chip, several polypeptides and/or antibodies of the invention of different specificity, and/or polypeptides and/or antibodies capable of recognizing microorganisms different from *Chlamydia pneumoniae*.

Accordingly, the subject of the present invention is also the polypeptides and the antibodies according to the invention, characterized in that they are immobilized on a support, in

10 particular of a protein chip.

The protein chips, characterized in that they contain at least one polypeptide or one antibody according to the invention immobilized on the support of the said chip, also form part of the invention.

The invention comprises, in addition, a protein chip according to the invention,

15 characterized in that it contains, in addition, at least one polypeptide of a microorganism different from *Chlamydia pneumoniae* or at least one antibody directed against a compound of a microorganism different from *Chlamydia pneumoniae*, immobilized on the support of the said chip.

The invention also relates to a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, or for the

20 detection and/or the identification of a microorganism characterized in that it comprises a protein chip according to the invention.

The subject of the present invention is also a method for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism in a biological sample, characterized in that it uses a nucleotide sequence according to

25 the invention.

More particularly, the invention relates to a method for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism in a biological sample, characterized in that it comprises the following steps:

a)   where appropriate, isolation of the DNA from the biological sample to be analysed, or optionally

30   production of a cDNA from the RNA in the biological sample;

b)   specific amplification of the DNA of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism with the aid of at least one primer according to the invention;

c)   detection of the amplification products.

35   These may be detected, for example, by the molecular hybridization technique using a nucleic probe according to the invention. This probe will be advantageously labelled with a nonradioactive (cold probe) or radioactive element.

For the purposes of the present invention, "DNA in the biological sample" or "DNA contained in the biological sample" will be understood to mean either the DNA present in the biological sample considered, or optionally the cDNA obtained after the action of a reverse transcriptase-type enzyme on the RNA present in the said biological sample.

Another aim of the present invention consists in a method according to the invention, characterized in that it comprises the following steps:

a)   bringing a nucleotide probe according to the invention into contact with a biological sample, the DNA contained in the biological sample having, where appropriate, been previously made accessible to hybridization, under conditions allowing the hybridization of the probe to complementary base pairs of the DNA of a bacterium belonging to the species *Chlamydia pneumoniae* or to an associated microorganism;

b)   detecting the hybridization complex formed between the nucleotide probe and the DNA in the biological sample.

The present invention also relates to a method according to the invention, characterized in that it comprises the following steps:

a)   bringing a nucleotide probe immobilized on a support according to the invention into contact with a biological sample, the DNA in the sample having, where appropriate, been previously made accessible to hybridization, under conditions allowing the hybridization of the probe to the DNA of a bacterium belonging to the species *Chlamydia pneumoniae* or to an associated microorganism;

b)   bringing the hybrid formed between the nucleotide probe immobilized on a support and the DNA contained in the biological sample, where appropriate after removal of the DNA in the biological sample which has not hybridized with the probe, into contact with a labelled nucleotide probe according to the invention;

c)   detecting the new hybrid formed in step b).

According to an advantageous embodiment of the method for the detection and/or the identification defined above, it is characterized in that, prior to step a), the DNA in the biological sample is primer-extended and/or amplified beforehand with the aid of at least one primer according to the invention.

The invention relates, in addition, to a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, characterized in that it comprises the following components:

a)   a nucleotide probe according to the invention;

b)   where appropriate, the reagents necessary for carrying out a hybridization reaction;

c)   where appropriate, at least one primer according to the invention as well as the reagents (e.g., polymerase and/or deoxynucleotide triphosphates) necessary for a DNA amplification reaction.

The invention also relates to a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, characterized in that it comprises the following components:

a)   a nucleotide probe, called capture probe, according to the invention;

5 b)   an oligonucleotide probe, called detection probe, according to the invention;

c)   where appropriate, at least one primer according to the invention as well as the reagents (e.g., polymerase and/or deoxynucleotide triphosphates) necessary for a DNA amplification reaction.

The invention also relates to a kit or set for the detection and/or the identification of 10 bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, characterized in that it comprises the following components:

a)   at least one primer according to the invention;

b)   where appropriate, the reagents necessary for carrying out a DNA amplification reaction;

c)   where appropriate, a component which makes it possible to check the sequence of the amplified 15   ·   fragment, more particularly an oligonucleotide probe according to the invention.

The invention relates, in addition, to a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, or for the detection and/or the identification of a microorganism characterized in that it comprises a DNA chip according to the invention.

20   The invention also relates to a method or to a kit or set according to the invention for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae*, characterized in that the said primer and/or the said probe according to the invention are chosen from the nucleotide sequences specific to the species *Chlamydia pneumoniae*, in that the said polypeptides according to the invention are chosen from the polypeptides specific to the species *Chlamydia* 25 *pneumoniae* and in that the said antibodies according to the invention are chosen from the antibodies directed against the polypeptides according to the invention chosen from the polypeptides specific to the species *Chlamydia pneumoniae*.

Preferably, the said method or the said kit or set above according to the invention, for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* is 30 characterized in that the said primer and/or the said probe or the said polypeptides are chosen from the nucleotide sequences or polypeptides according to the invention which have been identified as being specific to the species *Chlamydia pneumoniae* and in that the said antibodies according to the invention are chosen from the antibodies directed against the polypeptides according to the invention chosen from the polypeptides identified as being specific to the species *Chlamydia pneumoniae*.

35   The invention relates, in addition, to a method or a kit or set according to the invention for the diagnosis of predispositions to, or of a condition caused by, cardiovascular diseases, preferably linked to the presence of atheroma, which are induced or worsened by a *Chlamydia pneumoniae*

66

infection.

The invention also relates to a method or a kit or set according to the invention for the diagnosis of predispositions to, or of conditions caused by, respiratory diseases induced or worsened by a *Chlamydia pneumoniae* infection; preferably, the said respiratory disease is asthma.

5   According to another aspect, the subject of the invention is the use of polypeptides according to the invention, of cells transformed with a vector according to the invention and/or of transformed animals according to the invention, for the biosynthesis or the biodegradation of organic or inorganic compounds.

As has been mentioned above, the nucleotide sequences of the invention were identified 10 by homology with sequences known to encode, for example, polypeptides or fragments of enzymatic polypeptides involved in the biosynthesis or the biodegradation of organic or inorganic molecules.

It is thus possible to use the said polypeptides of the invention in a similar manner for the biosynthesis or the biodegradation of organic or inorganic compounds of industrial or therapeutic interest (called compounds of interest).

15   Among these polypeptides, there may be mentioned in particular the enzymes involved in metabolism, such as the proteolytic enzymes, amino transferases, glucose metabolism, or the enzymes which may be used in the biosynthesis of sugars, amino acids, fatty acids, polypeptides, nucleotides, nucleic acids or any other organic or inorganic compound or in the biodegradation of organic or inorganic compounds.

20   Among these polypeptides, there may be mentioned, in addition, the mutated or modified enzymes corresponding to mutated or modified polypeptides according to the invention which may also be used for the biosynthesis or the biodegradation of organic or inorganic compounds at the industrial level, such as, for example, the production of compounds of interest, the reprocessing of manufacturing residues applied to the food industries, to the papermaking industry or to the chemical 25 and pharmaceutical industries.

The methods of biosynthesis or biodegradation of organic or inorganic compounds, characterized in that they use a polypeptide or one of its representative fragments according to the invention, transformed cells according to the invention and/or a transformed animal according to the invention, also form part of the invention.

30   The invention relates, in addition, to the use of a nucleotide sequence according to the invention, of a polypeptide according to the invention, of an antibody according to the invention, of a cell according to the invention, and/or of a transformed animal according to the invention, for the selection of an organic or inorganic compound capable of modulating, regulating, inducing or inhibiting the expression of genes, and/or of modifying the cellular replication of eukaryotic or 35 prokaryotic cells or capable of inducing, inhibiting or worsening the pathologies linked to an infection by *Chlamydia pneumoniae* or one of its associated microorganisms.

The invention also comprises screening assays that comprise methods of selecting

compounds capable of binding to a polypeptide, fusion polypeptide or one of its representative fragments according to the invention, capable of binding to a nucleotide sequence according to the invention, or capable of recognizing an antibody according to the invention, and/or capable of modulating, regulating, inducing or inhibiting the expression of genes, and/or of modifying the growth or the cellular replication of eukaryotic or prokaryotic cells, or capable of inducing, inhibiting or worsening, in an animal or human organism, the pathologies linked to an infection by *Chlamydia pneumoniae* or one of its associated microorganisms, characterized in that it comprises the following steps:

a) bringing the said compound into contact with the said polypeptide, the said nucleotide sequence, with a transformed cell according to the invention and/or administering the said compound to a transformed animal according to the invention;

b) determining the capacity of the said compound to bind with the said polypeptide or the said nucleotide sequence, or to modulate, regulate, induce or inhibit the expression of genes, or to modulate growth or cellular replication, or to induce, inhibit or worsen in the said transformed animal, the pathologies linked to an infection by *Chlamydia pneumoniae* or one of its associated microorganisms.

The transformed cells and/or animals according to the invention may advantageously serve as a model and may be used in methods for studying, identifying and/or selecting compounds capable of being responsible for pathologies induced or worsened by *Chlamydia pneumoniae*, or capable of preventing and/or of treating these pathologies such as, for example, cardiovascular or respiratory diseases. In particular, the transformed host cells, in particular bacteria of the *Chlamydia* family whose transformation with a vector according to the invention may, for example, increase or inhibit its infectivity, or modulate the pathologies usually induced or worsened by the infection, may be used to infect animals in which the onset of pathologies will be monitored. These nontransformed animals, infected for example with transformed *Chlamydia* bacteria, may serve as a study model. In the same manner, the transformed animals according to the invention may, for example, exhibit predispositions to cardiovascular and/or respiratory diseases and thus be used in methods for selecting compounds capable of preventing and/or of treating the said diseases. The said methods using the said transformed cells and/or transformed animals form part of the invention.

The compounds capable of being selected may be organic compounds such as polypeptides or carbohydrates or any other organic or inorganic compounds already known, or new organic compounds produced using molecular modeling techniques and obtained by chemical or biochemical synthesis, these techniques being known to persons skilled in the art.

The said selected compounds may be used to modulate the growth and/or the cellular replication of *Chlamydia pneumoniae* or any other associated microorganism and thus to control infection by these microorganisms. The said compounds according to the invention may also be used to modulate the growth and/or the cellular replication of all eukaryotic or prokaryotic cells, in

particular tumour cells and infectious microorganisms, for which the said compounds will prove active, the methods which make it possible to determine the said modulations being well known to persons skilled in the art.

Compound capable of modulating the growth of a microorganism is understood to
5   designate any compound which makes it possible to act, to modify, to limit and/or to reduce the development, the growth, the rate of proliferation and/or the viability of the said microorganism.

This modulation may be achieved, for example, by an agent capable of binding to a protein and thus of inhibiting or of potentiating its biological activity, or capable of binding to a membrane protein of the outer surface of a microorganism and of blocking the penetration of the said
10 microorganism into the host cell or of promoting the action of the immune system of the infected organism directed against the said microorganism. This modulation may also be achieved by an agent capable of binding to a nucleotide sequence of a DNA or RNA of a microorganism and of blocking, for example, the expression of a polypeptide whose biological or structural activity is necessary for the growth or for the reproduction of the said microorganism.

15   Associated microorganism is understood to designate in the present invention any microorganism whose gene expression may be modulated, regulated, induced or inhibited, or whose growth or cellular replication may also be modulated by a compound of the invention. Associated microorganism is also understood to designate in the present invention any microorganism containing nucleotide sequences or polypeptides according to the invention. These microorganisms may, in some
20 cases, contain polypeptides or nucleotide sequences identical or homologous to those of the invention may also be detected and/or identified by the detection and/or identification methods or kit according to the invention and may also serve as a target for the compounds of the invention.

The invention relates to the compounds capable of being selected by a method of selection according to the invention.

25   The invention also relates to a pharmaceutical composition comprising a compound chosen from the following compounds:

a nucleotide sequence according to the invention;

a polypeptide according to the invention;

a vector according to the invention;

30 an antibody according to the invention; and

a compound capable of being selected by a method of selection according to the invention, optionally
        in combination with a pharmaceutically acceptable vehicle.

An effective quantity is understood to designate a sufficient quantity of the said compound or antibody, or of a polypeptide of the invention, which makes it possible to modulate the
35 growth of *Chlamydia pneumoniae* or of an associated microorganism.

The invention also relates to a pharmaceutical composition comprising one or more polypeptides according to the invention and/or one or more fusion polypeptides according to the

69

invention. Such compositions further comprise a pharmaceutically acceptable carrier or vehicle. Pharmaceutical compositions include compositions that comprise a polypeptide or fusion polypeptide that immunoreacts with seropositive serum of an individual infected with *Chlamydia pneumoniae*. In one embodiment, a pharmaceutical composition according to the invention can be utilized for the

5   prevention or the treatment of an infection by a bacterium belonging to the species *Chlamydia pneumoniae* or by an associated microorganism.

The invention relates, in addition, to an immunogenic composition or a vaccine composition, characterized in that it comprises one or more polypeptides according to the invention and/or one or more hybrid (fusion) polypeptides according to the invention. Such compositions

10   further comprise a pharmaceutically acceptable carrier or vehicle. Immunogenic compositions or fusion polypeptide include compositions that comprise a polypeptide that immunoreacts with seropositive serum of an individual infected with *Chlamydia pneumoniae*.

Immunogenic or vaccine compositions can also comprise DNA immunogenic or vaccine compositions comprising polynucleotide sequences of the invention operatively associated with a

15   regulatory sequence that controls gene expression. Such compositions can include compositions that direct expression of a neutralizing epitope of *Chlamydia pneumoniae*.

The invention also comprises the use of a transformed cell according to the invention, for the preparation of a vaccine composition.

The invention also relates to a vaccine composition, characterized in that it contains a

20   nucleotide sequence according to the invention, a vector according to the invention and/or a transformed cell according to the invention.

The invention also relates to the vaccine compositions according to the invention, for the prevention or the treatment of an infection by a bacterium belonging to the species *Chlamydia pneumoniae* or by an associated microorganism.

25   The invention also relates to the use of DNA encoding polypeptides of *Chlamydia pneumoniae*, in particular antigenic determinants, to be formulated as vaccine compositions. In accordance with this aspect of the invention, the DNA of interest is engineered into an expression vector under the control of regulatory elements, which will promote expression of the DNA, *i.e.*, promoter or enhancer elements. In one preferred embodiment, the promoter element may be cell-

30   specific and permit substantial transcription of the DNA only in predetermined cells. The DNA may be introduced directly into the host either as naked DNA (U.S. Patent No. 5,679,647 incorporated herein by reference in their entirety) or formulated in compositions with other agents which may facilitate uptake of the DNA including viral vectors, *i.e.*, adenovirus vectors, or agents which facilitate immunization, such as bupivicaine and other local anesthetics (U.S. Patent 5,593,972 incorporated

35   herein by reference in their entirety), saponins (U.S. Patent 5,739,118 incorporated herein by reference in their entirety) and cationic polyamines (published international application WO 96/10038 incorporated herein by reference in their entirety).

The DNA sequence encoding the antigenic polypeptide and regulatory element may be inserted into a stable cell line or cloned microorganism, using techniques, such as targeted homologous recombination, which are well known to those of skill in the art, and described *e.g.*, in Chappel, U.S. Patent No. 4,215,051; Skoultchi, WO 91/06667 each of which is incorporated herein by 5 reference in its entirety.

Such cell lines and microorganisms may be formulated for vaccine purposes. In yet another embodiment, the DNA sequence encoding the antigenic polypeptide and regulatory element may be delivered to a mammalian host and introduced into the host genome via homologous recombination (*See*, Chappel, U.S. Patent No. 4,215,051; Skoultchi, WO 91/06667 each of which is 10 incorporated herein by reference in its entirety.

Preferably, the immunogenic and/or vaccine compositions according to the invention intended for the prevention and/or the treatment of an infection by *Chlamydia pneumoniae* or by an associated microorganism will be chosen from the immunogenic and/or vaccine compositions comprising a polypeptide or one of its representative fragments corresponding to a protein, or one of 15 its · representative fragments, of the cellular envelope of *Chlamydia pneumoniae*. The vaccine compositions comprising nucleotide sequences will also preferably comprise nucleotide sequences encoding a polypeptide or one of its representative fragments corresponding to a protein, or one of its representative fragments, of the cellular envelope of *Chlamydia pneumoniae*.

Among these preferred immunogenic and/or vaccine compositions, the most preferred are 20 those comprising a polypeptide or one of its representative fragments, or a nucleotide sequence or one of its representative fragments whose sequences are chosen from the nucleotide or amino acid sequences identified in this functional group and listed above.

The polypeptides of the invention or their representative fragments entering into the immunogenic compositions according to the invention may be selected by techniques known to 25 persons skilled in the art, such as for example on the capacity of the said polypeptides to stimulate T cells, which results, for example, in their proliferation or the secretion of interleukins, and which leads to the production of antibodies directed against the said polypeptides.

In mice, in which a weight dose of the vaccine composition comparable to the dose used in humans is administered, the antibody reaction is tested by collecting serum followed by a study of 30 the formation of a complex between the antibodies present in the serum and the antigen of the vaccine composition, according to the customary techniques.

According to the invention, the said vaccine compositions will be preferably in combination with a pharmaceutically acceptable vehicle and, where appropriate, with one or more appropriate immunity adjuvants.

35 Various types of vaccines are currently available for protecting humans against infectious diseases: attenuated live microorganisms (*M. bovis* - BCG for tuberculosis), inactivated microorganisms (influenza virus), acellular extracts (*Bordetella pertussis* for whooping cough),

recombinant proteins (hepatitis B virus surface antigen), polysaccharides (pneumococci). Experiments are underway on vaccines prepared from synthetic peptides or from genetically modified microorganisms expressing heterologous antigens. Even more recently, recombinant plasmid DNAs carrying genes encoding protective antigens were proposed as an alternative vaccine strategy. This

5 type of vaccination is carried out with a particular plasmid derived from an *E. coli* plasmid which does not replicate *in vivo* and which encodes only the vaccinal protein. Animals were immunized by simply injecting the naked plasmid DNA into the muscle. This technique leads to the expression of the vaccine protein *in situ* and to a cell-type (CTL) and a humoral type (antibody) immune response. This double induction of the immune response is one of the main advantages of the technique of

10 vaccination with naked DNA.

        The vaccine compositions of the present invention can be evaluated in *in vitro* and *in vivo* animal models prior to host, e.g., human, administration. For example, *in vitro* neutralization assays such as those described by Peterson et al. (1988) can be utilized. The assay described by Peterson et al. (1988) is suitable for testing vaccine compositions directed toward either *Chlamydia pneumoniae*

15 or *Chlamydia trachomatis*.

        Briefly, hyper-immune antisera is diluted in PBS containing 5% guinea pig serum, as a complement source. *Chlamydiae* (10^4 IFU; infectious units) are added to the antisera dilutions. The antigen-antibody mixtures are incubated at 37EC for 45 minutes and inoculated into duplicate confluent Hep-2 or HeLa cell monolayers contained in glass vials (e.g., 15 by 45 mm), which have

20 been washed twice with PBS prior to inoculation. The monolayer cells are infected by centrifugation at 1000X g for 1 hour followed by stationary incubation at 37E for 1 hour. Infected monolayers are incubated for 48 or 72 hours, fixed and stained with a *Chlamydiae* specific antibody, such as anti-MOMP for *C.trachomatis, etc.* IFUs are counted in ten fields at a magnification of 200X. Neutralization titer is assigned based on the dilution that gives 50% inhibition as compared to control

25 monolayers/IFU.

        The efficacy of vaccine compositions can be determined *in vivo* by challenging animal models of *Chlamydia pneumoniae* infection, e.g., mice or rabbits, with the vaccine compositions. For example, *in vivo* vaccine composition challenge studies can be performed in the murine model of *Chlamydia pneumonia* infection described by Moazed et al. (1997). Briefly, male homozygous apoE

30 deficient and/or C57 BL/6J mice are immunized with vaccine compositions. Post-vaccination, the mice are mildly sedated by subcutaneous injection of a mixture of ketamine and xylazine, and inoculated intranasally with a total volume of 0.03-0.05 ml of organisms suspended in SPG medium or with SPG alone. The inoculations of *Chlamydia pneumoniae* are approximately 3×10^7 IFU/mouse. The mice are inoculated with *Chlamydia pneumoniae* at 8, 10, and 12 weeks of age. Tissues are then

35 collected from the lung, spleen, heart, etc. at 1-20 weeks after the first inoculation. The presence of organisms is scored using PCR, histology and immunocytochemistry, or by quantitative culture/IFU after tissue homogenization.

Alternatively, *in vivo* vaccine composition challenge studies can be performed in the rabbit model of *Chlamydia pneumoniae* described by Laitinen et al. (1997). Briefly, New Zealand white rabbits (5 months old) are immunized with the vaccine compositions. Post-vaccination, the rabbits are sedated with Hypnorm, 0.3 ml/Kg of body weight, intramuscularly, and inoculated

5   intranasally with a total of 0.5 ml of *Chlamydia pneumoniae* suspended in SPG medium or with SPG alone. The inoculations of *Chlamydia pneumoniae* are approximately 3×10^7 IFU/rabbit. The rabbits are reinfected in the same manner and with the same dose 3 weeks after the primary inoculation. Tissues are then collected 2 weeks after the primary infection and 1, 2, and 4 weeks after the reinfection. The presence of *Chlamydia pneumoniae* is scored using PCR, histology and

10   immunocytochemistry, or by quantitative culture/IFU after tissue homogenization.

The vaccine compositions comprising nucleotide sequences or vectors into which the said sequences are inserted are in particular described in International Application No. WO 90/11092 and also in International Application No. WO 95/11307.

The nucleotide sequence constituting the vaccine composition according to the invention

15   may be injected into the host after having been coupled to compounds which promote the penetration of this polynucleotide inside the cell or its transport up to the cell nucleus. The resulting conjugates may be encapsulated into polymeric microparticles, as described in International Application No. WO 94/27238 (Medisorb Technologies International).

According to another embodiment of the vaccine composition according to the invention,

20   the nucleotide sequence, preferably a DNA, is complexed with the DEAE-dextran (Pagano et al., 1967) or with nuclear proteins (Kaneda et al., 1989), with lipids (Felgner et al., 1987) or encapsulated into liposomes (Fraley et al., 1980) or alternatively introduced in the form of a gel facilitating its transfection into the cells (Midoux et al., 1993, Pastore et al., 1994). The polynucleotide or the vector according to the invention may also be in suspension in a buffer solution or may be combined with

25   liposomes.

Advantageously, such a vaccine will be prepared in accordance with the technique described by Tacson et al. or Huygen et al. in 1996 or alternatively in accordance with the technique described by Davis et al. in International Application No. WO 95/11307.

Such a vaccine may also be prepared in the form of a composition containing a vector

30   according to the invention, placed under the control of regulatory elements allowing its expression in humans or animals. It is possible, for example, to use, as vector for the *in vivo* expression of the polypeptide antigen of interest, the plasmid pcDNA3 or the plasmid pcDNA1/neo, both marketed by Invitrogen ® & D Systems, Abingdon, United Kingdom). It is also possible to use the plasmid V1Jns.tPA, described by Shiver et al. in 1995. Such a vaccine will advantageously comprise, in

35   addition to the recombinant vector, a saline solution, for example a sodium chloride solution.

The immunogenic compositions of the invention can also be utilized as part of methods for immunization, wherein such methods comprise administering to a host, e.g., a human host, an

immunizing amount of the immunogenic compositions of the invention. In a preferred embodiment, the method of immunizing is a method of immunizing against *Chlamydia pneumoniae*.

A pharmaceutically acceptable vehicle is understood to designate a compound or a combination of compounds entering into a pharmaceutical or vaccine composition which does not
5   cause side effects and which makes it possible, for example, to facilitate the administration of the active compound, to increase its life and/or its efficacy in the body, to increase its solubility in solution or alternatively to enhance its preservation. These pharmaceutically acceptable vehicles are well known and will be adapted by persons skilled in the art according to the nature and the mode of administration of the active compound chosen.

10 As regards the vaccine formulations, these may comprise appropriate immunity adjuvants which are known to persons skilled in the art, such as, for example, aluminum hydroxide, a representative of the family of muramyl peptides such as one of the peptide derivatives of N-acetyl-muramyl, a bacterial lysate, or alternatively incomplete Freund's adjuvant, Stimulon™ QS-21 (Aquila Biopharmaceuticals, Inc., Framingham, MA), MPL™ (3-O-deacylated monophosphoryl lipid A; RIBI
15 ImmunoChem Research, Inc., Hamilton, MT), aluminum phosphate, IL-12 (Genetics Institute, Cambridge, MA).

Preferably, these compounds will be administered by the systemic route, in particular by the intravenous route, by the intranasal, intramuscular, intradermal or subcutaneous route, or by the oral route. More preferably, the vaccine composition comprising polypeptides according to the
20 invention will be administered several times, spread out over time, by the intradermal or subcutaneous route.

Their optimum modes of administration, dosages and galenic forms may be determined according to criteria which are generally taken into account in establishing a treatment adapted to a patient, such as for example the patient's age or body weight, the seriousness of his general condition,
25 tolerance of the treatment and the side effects observed.

The invention comprises the use of a composition according to the invention for the treatment or the prevention of cardiovascular diseases, preferably linked to the presence of atheroma, which are induced or worsened by *Chlamydia pneumoniae*.

Finally, the invention comprises the use of a composition according to the invention for
30 the treatment or the prevention of respiratory diseases which are induced or worsened by the presence of *Chlamydia pneumoniae*, preferably asthma.

Other characteristics and advantages of the invention appear in the following examples and figures:

35 Legend to the figures :

Figure 1 : Line for the production of *Chlamydia pneumoniae* sequences

Figure 2 : Analysis of the sequences and assembling

Figure 3 : Finishing techniques

> Figure 3a) : Assembly map

> Figure 3b) : Determination and use of the orphan ends of the contigs

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EXAMPLES

Experimental procedures

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Cells

The *Chlamydia pneumoniae* strain (CM1) used by the inventors is obtained from ATCC (American Culture Type Collection) where it has the reference number ATCC 1360-VR.

It is cultured on HeLa 229 cells, obtained from the American Type Culture Collection,
15   under the reference ATCC CCL-2.1.

Culture of the cells

The HeLa ATCC CCL-2.1 cells are cultured in 75-ml cell culture flasks (Corning). The culture medium is Dulbecco's modified cell culture medium (Gibco BRL No. 04101965) supplemented with MEM amino acids (Gibco BRL - No. 04301140) L (5 ml per 500 ml of medium)
20   and 5% foetal calf serum (Gibco BRL No. 10270 batch 40G8260K) without antibiotics or antifungals.

The cell culture stock is maintained in the following manner. The cell cultures are examined under an inverted microscope. 24 hours after confluence, each cellular lawn is washed with PBS (Gibco BRL No. 04114190), rinsed and then placed for 5 min in an oven in the presence of 3 ml of trypsine (Gibco BRL No. 25200056). The cellular lawn is then detached and then resuspended in
25   120 ml of culture medium, the whole is stirred in order to make the cellular suspension homogeneous. 30 ml of this suspension are then distributed per cell culture flask. The flasks are kept in a CO_2 oven (5%) for 48 hours at a temperature of 37°C. The cell stock is maintained so as to have available daily 16 flasks of subconfluent cells. It is these subconfluent cells which will be used so as to be infected with Chlamydia. 25-ml cell culture flasks are also used, these flasks are prepared in a similar manner
30   but the volumes used for maintaining the cells are the following: 1 ml of trypsine, 28 ml of culture medium to resuspend the cells, 7 ml of culture medium are used per 25-ml flask.

Infection of the cells with Chlamydia

Initially, the Chlamydiae are obtained frozen from ATCC (-70°C), in suspension in a volume of 1 ml. This preparation is slowly thawed, 500 µl are collected and brought into contact with
35   subconfluent cells, which are obtained as indicated above, in a 25-ml cell culture flask, containing 1 ml of medium, so as to cover the cells. The flask is then centrifuged at 2000 rpm in a "swing" rotor for microtitre plates, the centrifuge being maintained at a temperature of 35°C. After centrifugation,

the two flasks are placed in an oven at 35°C for three hours. 6 ml of culture medium containing cycloheximide (1 µg/ml) are then added and the flask is stored at 35°C. After 72 hours, the level of infection is evaluated by direct immunofluorescence and by the cytopathogenic effect caused to the cells.

5   Direct immunofluorescence

Starting with infected cells, which were obtained as indicated above, a cellular smear is deposited with a Pasteur pipette on a microscope slide. The cellular smear is fixed with acetone for 10 minutes; after draining the acetone, the smear is covered with 30 µl of murine monoclonal antibodies directed against MOMP (major outer membrane protein) of Chlamydia (Syva, Biomérieux) labelled with fluorescein isothiocyanate. The whole is then incubated in a humid chamber at a temperature of 37°C. The slides are then rinsed with water, slightly dried, and then after depositing a drop of mounting medium, a coverslip is mounted before reading. The reading is carried out with the aid of a fluorescence microscope equipped with the required filters (excitation at 490 nm, emission at 520 nm).

15   Harvesting of the *Chlamydia pneumoniae*

After checking the infection by direct immunofluorescence, carried out as indicated above, the culture flasks are opened under a sterile cabinet, sterile glass beads with a diameter of the order of a millimeter are placed in the flask. The flask is closed and then vigorously stirred while being maintained horizontally, the cellular lawn at the bottom, so that the glass beads can have a mechanical action on the cellular lawn. Most of the cells are thus detached or broken; the effect of the stirring is observed under an optical microscope so as to ensure proper release of Chlamydiae.

Large-scale infection of the cell cultures

The product of the Chlamydiae harvest (culture medium and cellular debris) is collected with a pipette, and distributed into three cell culture flasks containing subconfluent HeLa ATCC CCL-2.1 cells, obtained as indicated above. The cells thus inoculated are placed under gentle stirring (swing) in an oven at 35°C. After one hour, the flasks are kept horizontally in an oven so that the culture medium covers the cells for 3 hours. 30 ml of culture medium containing actydione (1 µg/ml) are then added to each of the flasks. The culture flasks are then stored at 35°C for 72 hours. The cells thus infected are examined under an optical microscope after 24 hours, the cytopathogenic effect is evaluated by the appearance of cytoplasmic inclusions which are visible under an inverted optical microscope. After 72 hours, the vacuoles containing the Chlamydiae occupy the cytoplasm of the cell and push the cell nucleus sideways. At this stage, numerous cells are spontaneously destroyed and have left free elementary bodies in the culture medium. The Chlamydiae are harvested as described above and are either frozen at –80°C or used for another propagation.

35   Purification of the Chlamydiae

The product of the Chlamydia harvests is stored at -80°C and thawed on a water bath at

room temperature. After thawing, each tube is vigorously stirred for one minute and immersed for one minute in an ultrasound tank (BRANSON 1200); the tubes are then stirred by inverting before being centrifuged for 5 min at 2000 rpm. The supernatant is carefully removed and kept at cold temperature (ice). The supernatant is vigorously stirred and then filtered on nylon filters having pores of 5 microns in diameter on a support (Nalgene) allowing a delicate vacuum to be established under the nylon filter. For each filtration, three nylon filters are superposed; these filters are replaced after every 40 ml of filtrate. Two hundred milliliters of filtration product are kept at cold temperature, and then after stirring by inverting, are centrifuged at 10,000 rpm for 90 min, the supernatant is removed and the pellet is taken up in 10 ml of 10 mM Tris, vigorously vortexed and then centrifuged at 10,000 rpm for 90 min. The supernatant is removed and the pellet is taken up in a buffer (20 mM Tris pH 8.0, 50 mM KCl, 5 mM MgCl$_2$) to which 800 units of DNAse I (Boehringer) are added. The whole is kept at 37°C for one hour. One ml of 0.5 M EDTA is then added, the whole is vortexed and frozen at −20°C.

Preparation of the DNA

The Chlamydiae purified above are thawed and subjected to a proteinase K (Boehringer) digestion in a final volume of 10 ml. The digestion conditions are the following: 0.1 mg/ml proteinase K, 0.1 × SDS at 55EC, stirring every 10 min. The product of digestion is then subjected to a double extraction with phenol-chloroform, two volumes of ethanol are added and the DNA is directly recovered with a Pasteur pipette having one end in the form of a hook. The DNA is dried on the edge of the tube and then resuspended in 500 μl of 2 mM Tris pH 7.5. The DNA is stored at 4°C for at least 24 hours before being used for the cloning.

Cloning of the DNA

After precipitation, the DNA is quantified by measuring the optical density at 260 nm. Thirty μg of Chlamydia DNA are distributed into 10 tubes of 1.5 ml and diluted in 300 μl of water. Each of the tubes is subjected to 10 applications of ultrasound lasting for 0.5 sec in a sonicator (unisonix XL2020). The contents of the 10 tubes are then grouped and concentrated by successive extractions with butanol (Sigma B1888) in the following manner: two volumes of butanol are added to the dilute DNA mixture. After stirring, the whole is centrifuged for five minutes at 2500 rpm and the butanol is removed. This operation is repeated until the volume of the aqueous phase is less than 1 ml. The DNA is then precipitated in the presence of ethanol and of 0.5 M sodium acetate pH 5.4, and then centrifuged for thirty minutes at 15,000 rpm at cold temperature (4°C). The pellet is washed with 75% ethanol, centrifuged for five minutes at 15,000 rpm and dried at room temperature. A tenth of the preparation is analysed on a 0.8% agarose gel. Typically, the size of the DNA fragments thus prepared is between 200 and 8000 base pairs.

To allow the cloning of the DNA obtained, the ends are repaired. The DNA is distributed in an amount of 10 μg/tube, in the following reaction medium: 100 μl final volume, 1 × buffer

(Biolabs 201L), 0.5 µl BSA 0.05 mg/ml, 0.1 mM   dATP, 0.1 mM each of dGTP, dCTP or dTTP, 60,000 IU T4 DNA polymerase. The reaction is incubated for thirty minutes at 16°C. The contents of each of the tubes are then grouped before carrying out an extraction with phenol-chloroform and then precipitating the aqueous phase as described above. After this step, the DNA thus prepared is

5   phosphorylated. For that, the DNA is distributed into tubes in an amount of 10 µg per tube, and then in a final volume of 50 µl, the reaction is prepared in the following manner: 1 mM ATP, 1 × kinase buffer, 10 IU T4 polynucleotide kinase (Biolabs 201L). The preparation is incubated for thirty minutes at 37°C. The contents of the tubes are combined and a phenol-chloroform extraction and then a precipitation are carried out in order to precipitate the DNA. The latter is then suspended in 1 µl of

10   water and then the DNA fragments are separated according to their size on a 0.8% agarose gel (1 × TAE). The DNA is subjected to an electric field of 5 V/cm and then visualized on a UV table. The fragments whose size varies between 1200 and 2000 base pairs are selected by cutting out the gel. The gel fragment thus isolated is placed in a tube and then the DNA is purified with the Qiaex kit (20021 Qiagen), according to the procedure provided by the manufacturer.

15   Preparation of the vector

14 µg of the cloning vector pGEM-5Zf (Proméga P2241) are diluted in a final volume of 150 µl and are subjected to digestion with the restriction enzyme EcoRV 300 IU (Biolabs 195S) according to the protocol and with the reagents provided by the manufacturer. The whole is placed at 37°C for 150 min and then distributed in the wells of a 0.8% agarose gel subjected to an electric field

20   of 5 V/cm. The linearized vector is visualized on a UV table, isolated by cutting out the gel and then purified by the Qiaex kit (Qiagen 20021) according to the manufacturer's recommendations. The purification products are grouped in a tube, the volume is measured and then half the volume of phenol is added and the whole is vigorously stirred for 1 min. Half the volume of chloroform-isoamyl alcohol 24:1 is added and vigorously stirred for 1 min. The whole is centrifuged at 15,000 rpm for

25   5 min at 4°C, the aqueous phase is recovered and transferred into a tube. The DNA is precipitated in the presence of 0.3 M sodium acetate, pH 5.4 and 3 volumes of ethanol and placed at -20°C for 1 hour. The DNA is then centrifuged at 15,000 rpm for 30 min at 4°C, the supernatant is removed while preserving the pellet, washed twice with 70% ethanol. After drying at room temperature, the DNA is suspended in 25 µl of water.

30   Phosphorylation of the vector

25 µl of the vector prepared in the preceding step are diluted in a final volume of 500 µl of the following reaction mixture:

After repair, the DNA is subjected to a phenol-chloroform extraction and a precipitation, the pellet is then taken up in 10 µl of water, the DNA is quantified by measuring the optical density at

35   260 nm. The quantified DNA is ligated into the vector PGEm-5Zf(+) prepared by the restriction

78

enzyme EcoRV and dephosphorylated (see preparation of the vector). The ligation is carried out under three conditions which vary in the ratio between the number of vector molecules and the number of insert molecules. Typically, an equimolar ratio, a ratio of 1:3 and a ratio of 3:1 are used for the ligations which are, moreover, carried out under the following conditions: vector PGEm-5Zf(+)

5   25 ng, cut DNA, ligation buffer in a final volume of 20 μl with T4 DNA ligase (Amersham E70042X); the whole is then placed in a refrigerator overnight and then a phenol-chloroform extraction and a precipitation are carried out in a conventional manner. The pellet is taken up in 5 μl of water.

Transformation of the bacteria

Plating of the bacteria

10   Petri dishes containing LB Agar medium containing ampicillin (50 μg/ml), Xgal (280 μg/ml) [5-bromo-4-chloro-indolyl-beta-D-galactopyranoside (Sigma B-4252)], IPTG (140 μg/ml) [isopropyl-beta-D-thiogalactoside (Sigma I-6758)] are used, 50 and 100 μl of bacteria are plated for each of the ligations. The Petri dishes are placed upside down at 37°C for 15 to 16 hours in an oven. The number of "recombinant" positive clones is evaluated by counting the white colonies and

15   the blue colonies which are thought to contain the vector alone.

Evaluation of the "recombinant" positive clones

Ninety-four white colonies and two blue colonies are collected with the aid of sterile cones and are deposited at the bottom of the wells of plates designed for carrying out the amplification techniques. 30 μl of the following reaction mixture are added to each well: 1.7 mM MgCl$_2$, 0.2 mM

20   each of dATP, dCTP, dGTP and dTTP, two synthetic oligonucleotides corresponding to sequences flanking the cloning site on either side and orienting the synthesis of the DNA in a convergent manner (0.5 μM RP and PU primers, 1 U TAQ polymerase (GibcoBRL 18038-026)).

The colonies thus prepared are subjected to a temperature of 94°C for 5 min and then to 30 thermal cycles composed of the following steps: 94°C for 40 s, 50°C for 30 s, 72°C for 180 s. The

25   reaction is then kept for 7 min at 72°C and then kept at 4°C.

The amplification products are deposited on an agarose gel (0.8%), stained with ethidium bromide, subjected to electrophoresis, and then analysed on an ultraviolet table. The presence of an amplification fragment having a size greater than 500 base pairs indicates the presence of an insert. The bacterial clones are then prepared so as to study the sequence of their insert.

30   Sequencing

To sequence the inserts of the clones obtained as above, these were amplified by PCR on bacteria cultures carried out overnight using the primers for the vectors flanking the inserts. The sequence of the ends of these inserts (on average 500 bases on each side) was determined by automated fluorescent sequencing on an ABI 377 sequencer, equipped with the ABI Prism DNA

35   Sequencing Analysis software (version 2.1.2).

Analysis of the sequences

The sequences obtained by sequencing in a high-yield line (Figure 1) are stored in a database; this part of the production is independent of any treatment of the sequences. The sequences are extracted from the database, avoiding all the regions of inadequate quality, that is to say the regions for which uncertainties are observed on the sequence at more than 95%. After extraction,

5   the sequences are introduced into a processing line, the diagram of which is described in Figure 2. In a first path of this processing line, the sequences are assembled by the Gap4 software from R. Staden (Bonfield et al., 1995) (OS UNIX/SUN Solaris); the results obtained by this software are kept in the form of two files which will be used for a subsequent processing. The first of these files provides information on the sequence of each of the contigs obtained. The second file represents all the clones

10   participating in the composition of all the contigs as well as their positions on the respective contigs.

The second processing path uses a sequence assembler (TIGR-Asmg assembler UNIX/SUN Solaris); the results of this second processing path are kept in the form of a file in the TIGR-Asmg format which provides information on the relationship existing between the sequences selected for the assembly. This assembler is sometimes incapable of linking contigs whose ends

15   overlap over several hundreds of base pairs.

The results obtained from these two assemblers are compared with the aid of the BLAST program, each of the contigs derived from one assembly path being compared with the contigs derived from the other path.

For the two processing paths, the strict assembly parameters are fixed (95% homology,

20   30 superposition nucleotides). These parameters avoid 3 to 5% of the clones derived from eukaryotic cells being confused with sequences obtained from the clones derived from *Chlamydia pneumoniae*. The eukaryotic sequences are however preserved during the course of this project; the strategy introduced, which is described below, will be designed, inter alia, not to be impeded by these sequences derived from contaminating clones.

25   The results of these two assemblers are processed in a software developed for this project. This software operates on a Windows NT platform and receives, as data, the results derived from the STADEN software and/or the results derived from the TIGR-Asmg assembler, the software, results, after processing of the data, in the determination of an assembly map which gives the proximity relationship and the orientation of the contigs in relation to one another (Figure 3a). Using

30   this assembly map, the software determines all the primers necessary for finishing the project. This treatment, which will be detailed below, has the advantage of distinguishing the isolated sequences derived from the contaminations, by the DNA eukaryotic cells, of the small-sized sequences clearly integrated into the project by the relationships which they establish with contigs. In order to allow, without any risk of error, the arrangement and the orientation of the contigs in relation to one another,

35   a statistical evaluation of the accuracy of the names (naming) "naming" of sequence is made from the results of "contigation". This evaluation makes it possible to give each of the clone plates, as well as each of the subsets of plates, a weight which is inversely proportional to probable error rate existing in

the "naming" of the sequences obtained from this plate or from a subset of this plate. In spite of a low error rate, errors may occur throughout the steps of production of the clones and of the sequences. These steps are numerous, repetitive and although most of them are automated, others, like the deposition in the sequencers, are manual; it is then possible for the operator to make mistakes such as

5   the inversion of two sequences. This type of error has a repercussion on the subsequent processing of the data, by resulting in relationships (between the contigs) which do not exist in reality, then in attempts at directed sequencing between the contigs which will end in failure. It is because of this that the evaluation of the naming errors is of particular importance since it allows the establishment of a probabilistic assembly map from which it becomes possible to determine all the clones which will

10   serve as template to obtain sequences separating two adjacent contigs. Table 2 of parent U.S. application serial No. 60/107078 filed November 4, 1998 and French application 97-14673 filed November 21, 1997, each of which is incorporated by reference herein in its entirety, gives the clones and the sequences of the primers initially used during the initial operations.

     To avoid the step which consists in ordering and then preparing the clones by
15   conventional microbiological means, outer and inner primers oriented towards the regions not yet sequenced are defined by the software. The primers thus determined make it possible to prepare, by PCR, a template covering the nonsequenced region. It is the so-called outer primers (the ones most distant from the region to be sequenced) which are used to prepare this template. The template is then purified and a sequence is obtained on each of the two strands during 2 sequencing reactions which

20   each use one of the 2 inner primers. In order to facilitate the use of this approach, the two outer primers and the two inner primers are prepared and then stored on the same position of 4 different 96-well plates. The two plates containing the outer primers are used to perform the PCRs which will serve to prepare the templates. These templates will be purified on purification columns preserving the topography of the plates. Each of the sequences will be obtained using primers situated on one and

25   then on the other of the plates containing the inner primers. This distribution allows a very extensive automation of the process and results in a method which is simple to use for finishing the regions not yet sequenced. Table 3 of parent U.S. application serial No. 60/107078 filed November 4, 1998 and French application 97-14673 filed November 21, 1997, each of which is incorporated by reference herein in its entirety, gives the names and the sequences of the primers used for finishing *Chlamydia*

30   *pneumoniae*.

     Finally, a number of contigs exist in a configuration where one of their ends is not linked to any other contig end (Figure 3b) by a connecting clone relationship (a connecting clone is defined as a clone having one sequence end on a contig and the other end of its sequence on another contig; furthermore, this clone must be derived from a plate or a subset of plates with adequate naming

35   quality). For the *Chlamydia pneumoniae* project, this particular case occurred 24 times. Two adjacent PCR primers orienting the synthesis of the DNA towards the end of the consensus sequence are defined for each of the orphan ends of the consensus sequence. The primer which is closest to the end

of the sequence is called the inner primer whereas the primer which is more distant from the end of the sequence is called the outer primer. The outer primers are used to explore the mutual relationship between the orphan ends of the different contigs. The presence of a single PCR product and the possibility of amplifying this product unambiguously using the inner primers evokes the probable

5   relationship between the contigs on which the primers which allowed the amplification are situated. This relationship will be confirmed by sequencing and will allow the connection between the orphan ends of the consensus sequences. This strategy has made it possible to obtain a complete map of the *Chlamydia pneumoniae* chromosome and then to finish the project.

Quality control

10   All the bases not determined with certainty in the chromosomal sequence were noted and the density of uncertainties was measured on the entire chromosome. The regions with a high density of uncertainties were noted and the PCR primers spanning these regions were drawn and are represented in Table 4 of parent U.S. application serial No. 60/107078 filed November 4, 1998 and French application 97-14673 filed November 21, 1997 each of which is incorporated by reference

15   herein in its entirety.

The sequence of each of the PCR products was obtained with two operational primers different from the amplification primers. The sequences were obtained in both directions for all the PCRs (100% success).

Data banks

20   Local reorganizations of major public banks were used. The protein bank used consists of the nonredundant fusion of the Genpept bank (automated translation of GenBank, NCBI; Benson et al., 1996).

The entire BLAST software (public domain, Altschul et al., 1990) for searching for homologies between a sequence and protein or nucleic data banks was used. The significance levels

25   used depend on the length and the complexity of the region tested as well as the size of the reference bank. They were adjusted and adapted to each analysis.

The results of the search for homologies between a sequence according to the invention and protein or nucleic data banks are presented and summarized in Table 1 below.

30   Table 1: List of coding chromosome regions and homologies between these regions and the sequence banks.

Legend to Table 1: Open reading frames are identified with the GenMark software version 2.3A (GenePro), the template used is *Chlamydia pneumoniae* of order 4 on a length of 196 nucleotides with a window of 12 nucleotides and a minimum signal of 0.5. The reading frames

35   ORF2 to ORF 1137 are numbered in order of appearance on the chromosome, starting with ORF2 (ORF column). The positions of the beginning and of the end are then given in column 2 (position). When the position of the beginning is greater than the position of the end, this means that the region is

encoded by the strand complementary to the sequence which was given in the sequence SEQ ID No. 1.

All the putative products were subjected to a search for homology on GENPEPT (release 102 for SEQ ID No. 2 to SEQ ID No. 1137, and release 108 for SEQ ID No. 1138 to SEQ ID No. 5 1291 and SEQ ID No. 6844 to SEQ ID No. 6849) with the BLASTP software (Altschul et al. 1990). With, as parameters, the default parameters with the exception of the expected value E set at 10^{-5} (for SEQ ID No. 2 to SEQ ID No. 1137) and P value set at e^{-10} (for SEQ ID No. 1138 to SEQ ID No. 1291 and SEQ ID No. 6844 to SEQ ID No. 6849). Subsequently, only the identities greater than 30% (I% column) were taken into account. The description of the most homologous sequence is given in the 10 Homology column; the identifier for the latter sequence is given in the ID column and the animal species to which this sequence belongs is given in the Species column. The Homology score is evaluated by the sum of the blast scores for each region of homology and reported in the Score column.

Materials and Methods for transmembrane domains:

15   The DAS software was used as recommended by the authors (Cserzo et al., 1997).

This method uses, to predict the transmembrane domains, templates derived from a sampling of selected proteins. All the regions for which a "Cutoff" greater than 1.5 was found by the program were taken into account.

20   Additional ORF Finder Programs

For this analysis, two additional ORF finder programs were used to predict potential open reading frames of a minimum length of 74 amino acids; Glimmer (Salzberg, S.L., Delcher, A., Kasif, S., and W. White. 1998. Microbial gene identification using interpolated Markov models. Nucleic Acids Res. 26:544-548.), and an in-house written program. The in-house program used a very simple 25 search algorithm. The analysis required the that the genomic DNA sequence text be in the 5' to 3' direction, the genome is circular, and that TAA, TAG, and TGA are stop codons. The search parameters were as follows:

(1)   A search for an ORF that started with a GTG codon was performed. If no GTG codons were found, then a search for an ATG codon was performed. However, if a GTG codon was 30   found, then a search downstream for a ATG codon was performed. All start and stop nucleotide positions were recorded.

(2)   A search for an ORF that started with a TTG codon was performed. If no TTG codons were found, then a search for a ATG codon was performed. However, if a TTG codon was found, then a search downstream for a ATG codon was performed. All start and stop 35   nucleotide positions were recorded.

(3)   The analysis described in steps 1 and 2 were repeated for the opposite strand of DNA sequence.

(4)   A search for ORFs that determined all   ORF lengths using start and stop positions in the same reading frames was performed.

(5)   All ORFs whose DNA length was less than 225 nucleotides were eliminated from the search.

5   Surface Exposed Protein Search Criteria

Potential cell surface vaccine targets are outer membrane proteins such as porins, lipoproteins, adhesions and other non-integral proteins. In *Chlamydia psittaci*, the major immunogens is a group of putative outer membrane proteins (POMPs) and no homologs have been found in *Chlamydia pneumoniae* and *Chlamydia trachomatis* by traditional analysis (Longbottom, D., Russell, 10   M., Dunbar, S.M., Jones, G.E., and A.J. Herring. 1998. Molecular Cloning and Characterization of the Genes Coding for the Highly Immunogenic Cluster of 90-Kilodalton Envelope Proteins from *Chlamydia psittaci* Subtype That Causes Abortion in Sheep. Infect Immun 66:1317-1324.) Several putative outer membrane proteins have been identified in *Chlamydia pneumoniae*, all of which may represent vaccine candidates. The major outer membrane protein (MOMP) gene (omp1) has been 15   found in various isolates of *Chlamydia pneumoniae* (Jantos, CA., Heck, S., Roggendorf, R., Sen-Gupta, M., and Hegemann, JH. 1997. Antigenic and molecular analyses of different chlamydia pneumoniae strains. J. Clin Microbiology 35(3):620-623.) Various criteria, as listed below, were used to identify putative surface exposed ORFs from the genomic DNA sequence of *Chlamydia pneumoniae* (French application 97-14673 filed 21 November 1997). Any ORF which met any one or 20   more of the individual criteria were listed in this category.

Protein homology searches were done using the Blastp 2.0 tool (Altschul, S.F., Madden, T.L., Schaffer, A.A., Zhang, J., Zhang, Z., Miller, W., and D.J. Lipman. 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402.)   An ORF product was labeled surface exposed if there was homology to a known, or 25   hypothetical, or putative surface exposed protein with a P score better than e^{-10} .

Most, if not all, proteins that are localized to the membrane of bacteria, via a secretory pathway, contain a signal peptide. A software program, SignalP, analyzes the amino acid sequence of an ORF for such a signal peptide (Nielsen, H., Engelbrecht. J., Brunak, S., and G. von Heijne. 1997. Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites. 30   Protein Engineering 10:1-6.) The first 60 N-terminal amino acids of each ORF were analyzed by SignalP using the Gram-Negative software database. The output generates four separate values, maximum C, maximum Y, maximum S, and mean S. The S-score, or signal region, is the probability of the position belonging to the signal peptide. The C-score, or cleavage site, is the probability of the position being the first in the mature protein. The Y-score is the geometric average of the C-score and 35   a smoothed derivative of the S-score. A conclusion of either a Yes or No is given next to each score. If all four conclusions are Yes and the C-terminal amino acid is either a phenylalanine (F) or a tyrosine (Y), the ORF product was labelled outer membrane (Struyve, M., Moons, M., and J. Tommassen.

1991. Carboxy-terminal Phenylalanine is Essential for the Correct Assembly of a Bacterial Outer Membrane Protein. J. Mol. Biol. 218:141-148.)

The program called Psort, determines the localization of a protein based on its signal sequence, recognition of transmembrane segments, and analysis of its amino acid composition (Nakai, K., and M. Kanehisa. 1991. Expert system for predicting protein localization sites in gram-negative bacteria. Proteins 11:95-110.) An ORF product is considered to be an outer membrane protein if the output data predicts the protein as outer membrane with a certainty value of 0.5 or better and whose value is at least twice as large as the next predicted localized certainty value.

Finally, ORF products that were not predicted to be outer membrane or surface exposed, based on the above criteria, were further analyzed. The blastp output data for these ORFs were searched using various general and specific keywords, suggestive of known cell surface exposed proteins. An ORF was labeled surface exposed if the keywords matched had a Blastp hit, had a P score better than e^{-10}, and that there was no better data indicating otherwise. The following is a list of the searched keywords:

Adhesion	Adhesin	Invasin	Invasion	Extensin	
Omp	Outer Surface	Porin	Outer Membrane		
Cell Surface	Cell Wall	Pilus	Pilin	Flagellar sheath	BtuB
Cir	ChuA	CopB	ExeD	FadL	FecA
FepA	FhuA	FmdC	FomA	FrpB	GspD
HemR	HgbA	Hgp	HmbR	HmuR	HMW
HrcC	Hrp	InvG	LamB	LbpA	LcrQ
Lmp1	MxiD	MOMP	PilE	HpaA	NolW
NspA	OpcP	OpnP	Opr	OspA	PhoE
PldA	Por	PscC	PulD	PupA	QuiX
RafY	ScrY	SepC	ShuA	SomA	SpiA
Tbp1	Yop	YscC	mip	Tol	

Those ORFs that did not meet the minimum requirement for being an outer membrane protein based on the above search criteria but which were homologous to identified outer membrane ORFs in *Chlamydia trachomatis* were included. The *Chlamydia trachomatis* genome (French patent applications FR97-15041, filed 28 November 1997 and 97-16034 filed 17 December 1997) was analyzed using the above search criteria and a number of outer membrane ORFs were identified. These *Chlamydia trachomatis* ORFs were then tested against the *Chlamydia pneumoniae* genome using Blastp. Any *Chlamydia pneumoniae* ORF with a Blastp P value better than e^{-10} against a *Chlamydia trachomatis* outer membrane was included in this section, if there was no better data

indicating otherwise. A list of ORFs in the *Chlamydia pneumoniae* genome encoding putative surface exposed proteins is set forth above in the specification.

Identification of Putative Lipoproteins in the Genome of *Chlamydia pneumoniae*

Lipoproteins are the most abundant post-translationally modified bacterial secretory proteins (Pugsley, A. P.. 1993. The complete general secretory pathway in Gram-negative bacteria. Microbiol. Rev. 57:50-108). The characteristic features of lipoproteins are a thiol-linked diacylglyceride and an amine-linked monoacyl group on the cysteine that becomes the amino-terminal residue after signal peptide cleavage by Signal Peptidase II. (Pugsley, A. P.. 1993. The complete general secretory pathway in Gram-negative bacteria. Microbiol. Rev. 57:50-108). The identification of putative lipoproteins from the genomic sequencing of *Chlamydia pneumoniae* was done by examining the deduced amino acid sequence of identified ORFs for the presence of a signal peptide with a Signal Peptidase II cleavage site analogous to the consensus sequence for prolipoprotein modification and processing reactions (Hayashi, S., and H. C. Wu. 1992. Identification and characterization of lipid-modified proteins in bacteria, p. 261-285. *In* N. M. Hooper and A. J. Turner (ed.) Lipid modification of proteins: A practical approach. Oxford University Press, New York; Sutcliffe, I. C. and R. R. B. Russell. 1995. Lipoproteins of Gram-positive bacteria. J. Bacteriol. 177:1123-1128.).

Chlamydia pneumoniae ORFs were initially screened for the most basic of lipoprotein characteristics, a cysteine in the first 30 amino acids of the deduced protein. ORFs with a standard start codon (ATG, GTG, or TTG) and having one or more of the following characteristics were selected for direct analysis of their first 30 amino acids:

(a) Significant Signal P value (at least two out of the four values are Yes)

(b) PSORT value indicating membrane passage (IM-inner membrane, Peri-periplasm, or OM-outer membrane)

(c) Identification of the word lipoprotein among the ORF blastp data set.

(d) A Blastp value of $<e^{-10}$ with a putative lipoprotein from *Chlamydia trachomatis* (French applications 97-15041 filed 28 November 1997 and 97-16034 filed 17 December 1997).

The first 30 amino acids of each ORF in this set were analyzed for the characteristics commonly found in lipoprotein signal peptides (Pugsley, A. P.. 1993. The complete general secretory pathway in Gram-negative bacteria. Microbiol. Rev. 57:50-108; Hayashi, S., and H. C. Wu. 1992.

86

Identification and characterization of lipid- modified proteins in bacteria, p. 261-285. *In* N. M. Hooper and A. J. Turner (ed.) Lipid modification of proteins: A practical approach. Oxford University Press, New York; Sutcliffe, I. C. and R. R. B. Russell. 1995. Lipoproteins of Gram-positive bacteria. J. Bacteriol. 177:1123-1128.) Putative lipoprotein signal peptides were required to have a

5 cysteine between amino acid 10 and 30 and reach a minimum score of three based on the following criteria for lipoprotein signal peptides:

(a) Identification of specific amino acids in specific positions around the cysteine which are part of the consensus Signal Peptidase II cleavage site (Hayashi, S., and H. C. Wu. 1992. Identification and characterization of lipid-modified proteins in bacteria, p. 261-285. *In* N. M.

10 Hooper and A. J. Turner (ed.) Lipid modification of proteins: A practical approach. Oxford University Press, New York); Sutcliffe, I. C. and R. R. B. Russell. 1995. Lipoproteins of Gram-positive bacteria. J. Bacteriol. 177:1123-1128). Since the identification of the cleavage site is the most important factor in identifying putative lipoproteins, each correctly positioned amino acid contributed toward reaching the minimum score of three.   (b)   A hydrophobic

15 ·   region rich in alanine and leucine prior to the cleavage site (Pugsley, A. P.. 1993. The complete general secretory pathway in Gram-negative bacteria. Microbiol. Rev. 57:50-108) contributed toward reaching the minimum score of three.

(c)   A short stretch of hydrophilic amino acids greater than or equal to 1 usually lysine or arginine following the N-terminal methionine (Pugsley, A. P.. 1993. The complete

20 general secretory pathway in Gram-negative bacteria. Microbiol. Rev. 57:50-108) contributed toward reaching the minimum score of three.

A list of ORFs in the *Chlamydia pneumoniae* genome encoding putative lipoproteins is set forth above in the specification.

25   <u>LPS-Related ORFs of *Chlamydia pneumoniae*</u>

Lipopolysaccharide (LPS) is an important major surface antigen of Chlamydia cells. Monoclonal antibodies (Mab) directed against LPS of *Chlamydia pneumoniae* have been identified that can neutralize the infectivity of *Chlamydia pneumoniae* both in vitro and in vivo (Peterson, E.M., de la Maza, L.M., Brade, L., Brade, H. 1998. Characterization of a Neutralizing Monoclonal

30 Antibody Directed at the Lipopolysaccharide of *Chlamydia pneumonia*. Infect. Immun. Aug. 66(8):3848-3855.) Chlamydial LPS is composed of lipid A and a core oligosaccharide portion and is phenotypically of the rough type (R-LPS) (Lukacova, M., Baumann, M., Brade, L., Mamat, U., Brade, H. 1994. Lipopolysaccharide Smooth-Rough Phase Variation in Bacteria of the Genus *Chlamydia*. Infect. Immun. June 62(6):2270-2276.) The lipid A component is composed of fatty acids

35 which serve to anchor LPS in the outer membrane. The core component contains sugars and sugar derivatives such as a trisaccharide of 3-deoxy-D-manno-octulosonic acid (KDO) (Reeves, P.R., Hobbs, M., Valvano, M.A., Skurnik, M., Whitfield, C., Coplin, D., Kido, N., Klena, J., Maskell, D.,

Raetz, C.R.H., Rick, P.D. 1996. *Bacterial Polysaccharide Synthesis and Gene Nomenclature* pp. 10071-10078, Elsevier Science Ltd.). The KDO gene product is a multifunctional glycosyltransferase and represents a shared epitope among the Chlamydia. For a review of LPS biosynthesis see, e.g., Schnaitman, C.A., Klena, J.D. 1993. Genetics of Lipopolysaccharide

5   Biosynthesis in Enteric Bacteria. Microbiol. Rev. 57:655-682.

A text search of the ORF blastp results identified several genes that are involved in Chlamydial LPS production with a P score better than e^{-10}. The following key-terms were used in the text search: KDO, CPS (Capsular Polysaccharide Biosynthesis), capsule, LPS, rfa, rfb, rfc, rfe, rha, rhl, core, epimerase, isomerase, transferase, pyrophosphorylase, phosphatase, aldolase, heptose,

10   manno, glucose, lpxB, fibronectin, fibrinogen, fucosyltransferase , lic, lgt, pgm, tolC, rol, ChoP, phosphorylcholine, waaF, PGL-Tb1. A list of ORFs in the *Chlamydia pneumoniae* genome encoding putative polypeptides involved in LPS biosynthesis is set forth above in the specification.

Type III And Other Secreted Products

15   Type III secretion enables gram-negative bacteria to secrete and inject pathogenicity proteins into the cytosol of eukaryotic host cells (Hueck, C. J., 1998. Type III Protein Secretion Systems in Bacterial Pathogens of Animals and Plants. In Microbiology and Molecular Biology Reviews. 62:379-433.) These secreted factors often resemble eukaryotic signal transduction factors, thus enabling the bacterium to redirect host cell functions (Lee, C.A., 1997. Type III secretion

20   systems: machines to deliver bacterial proteins into eukaryotic cells? Trends Microbiol. 5:148-156.) In an attempt to corrupt normal cellular functions, Chlamydial pathogenicity factors injected into the host cytosol will nonetheless, as cytoplasmic constituents be processed and presented in the context of the Major Histocompatibility Complex (MHC class I). As such, these pathogenicity proteins represent MHC class I antigens and will play an important role in cellular immunity. Also included in this set

25   are secreted non-type III products that may play a role as vaccine components.

A text search of the ORF blastp results identified genes that are involved in *Chlamydia pneumoniae* protein secretion with a P score better than e^{-10}. The following key-terms were used in the text search in an effort to identify surface localized or secreted products: Yop, Lcr, Ypk, Exo, Pcr, Pop, Ipa, Vir, Ssp, Spt, Esp, Tir, Hrp, Mxi, hemolysin, toxin, IgA protease, cytolysin, tox, hap,

30   secreted and Mip.

Chlamydia pneumoniae ORFs that did not meet the above keyword search criteria, but have homologs in *Chlamydia trachomatis* that do meet the search criteria are included herein. The *Chlamydia trachomatis* genome (French patent applications FR97-15041, filed 28 November 1997 and 97-16034 filed 17 December 1997) was analyzed using the above search criteria and a number of

35   ORFs were identified. These *Chlamydia trachomatis* ORFs were tested against the *Chlamydia pneumoniae* genome using Blastp. Any *Chlamydia pneumoniae* ORF with a Blastp P value $< e^{-10}$ against a *Chlamydia trachomatis* homolog, identified using the above search criteria, was included. A

list of ORFs in the *Chlamydia pneumoniae* genome encoding putative secreted proteins is in the specification.

Chlamydia pneumoniae: RGD Recognition Sequence

Proteins that contain Arg-Gly-Asp (RGD) attachment site, together with integrins that serve as their receptor constitute a major recognition system for cell adhesion. The RGD sequence is the cell attachment site of a large number of adhesive extracellular matrix, blood, and cell surface proteins and nearly half of the known integrins recognize this sequence in their adhesion protein ligands. There are many RGD containing microbial proteins such as the penton protein of adenovirus, the coxsackie virus, the foot and mouth virus and pertactin, a 69 kDa (kilodalton) surface protein of *Bordetella pertussis,* that serve as ligands through which these microbes bind to integrins on the cell surfaces and gain entry into the cell. The following provides evidence supporting the importance of RGD in microbial adhesion:

a) The adenovirus penton base protein has a cell rounding activity and when penton base was expressed in E. coli, it caused cell rounding and cells adhered to polystyrene wells coated with the protein. Mutant analysis showed that both these properties required an RGD sequence. Virus mutants with amino acid substitutions in the RGD sequence, showed much less adherence to HeLa S3 cells, and also were delayed in virus reproduction (Bai, M., Harfe, B., and Freimuth, P. 1993. Mutations That Alter an RGD Sequence in the Adenovirus Type 2 Penton Base Protein Abolish Its Cell-Rounding Activity and Delay Virus Reproduction in Flat Cells. J. Virol. 67:5198-5205).

b) It has been shown that attachment and entry of coxsackie virus A9 to GMK cells were dependent on an RGD motif in the capsid protein VP1. VP1 has also been shown to bind $\alpha_v\beta_3$ integrin, which is a vitronectin receptor (Roivainen, M., Piirainen, L., Hovi, T., Virtanen, I., Riikonen, T., Heino, J., and Hyypia, T. 1994. Entry of Coxsackievirus A9 into Host Cells: Specific Interactions with a,b₃ Integrin, the Vitronectin Receptor Virology, 203:357-65).

c) During the course of whooping cough, *Bordetella pertussis* interacts with alveolar macrophages and other leukocytes on the respiratory epithelium. Whole bacteria adheres by means of two proteins, filamentous hemagglutinin (FHA) and pertussis toxin. FHA interacts with two classes of molecules on macrophages, galactose containing glycoconjugates and the integrin CR3. The interaction between CR3 and FHA involves recognition of RGD sequence at the positions 1097-1099 in FHA (Relman, D., Tuomanen, E., Falkow, S., Golenbock, D. T., Saukkonen, K., and Wright, S. D. "Recognitition of a Bacterial Adhesin by an Integrin: Macrophage CR3 Binds Filamentous Hemagglutinin of Bordetella Pertussis." Cell, 61:1375-1382 (1990)).

d) Pertactin, a 69 kDa outer membrane protein of *Bordetella pertussis,* has been shown to promote attachment of Chinese hamster ovary cells (CHO). This attachment is mediated by recognition of RGD sequence in pertactin by integrins on CHO cells and can be inhibited by synthetic RGD containing peptide homologous to the one present in pertactin (Leininger, E., Roberts, M., Kenimer, J. G., Charles, I. G., Fairweather, N., Novotny, P., and Brennan, M. J. 1991. Pertactin, an Arg-Gly-Asp containing *Bordetella pertussis* surface protein that promotes adherence of mammalian cells Proc. Natl. Acad. Sci. USA, 88:345-349).

e) The RGD sequence is highly conserved in the VP1 protein of foot and mouth disease virus (FMDV). Attachment of FMDV to baby hamster kidney cells (BHK) has been shown to be mediated by VP1 protein via the RGD sequence. Antibodies against the RGD sequence of VP1 blocked attachment of virus to BHK cells (Fox, G., Parry, N. R., Barnett, P. V., McGinn, B., Rowland, D. J., and Brown, F. 1989. The Cell Attachment Site on Foot-and-Mouth Disease Virus Includes the Amino Acid Sequence RGD (Arginine-Glycine-Aspartic Acid) J. Gen. Virol., 70:625-637).

It has been demonstrated that bacterial adherence can be based on interaction of a bacterial adhesin RGD sequence with an integrin and that bacterial adhesins can have multiple binding site characteristic of eukaryotic extracellular matrix proteins. RGD recognition is one of the important mechanisms used by microbes to gain entry into eukaryotic cells.

The complete deduced protein sequence of the *Chlamydia pneumoniae* genome was searched for the presence of RGD sequence. There were a total of 54 ORFs that had one or more RGD sequences. Not all RGD containing proteins mediate cell attachment. It has been shown that RGD containing peptides that have proline immediately following the RGD sequence are inactive in cell attachment assays (Pierschbacher & Ruoslahti. 1987. Influence of stereochemistry of the sequence Arg-Gly-Asp-Xaa on binding specificity in cell adhesion. J. Biol. Chem. 262:17294-98). ORFs that had RGD, with proline as the amino acid following the RGD sequence were excluded from the list. Also, RGD sequence may not be available at the surface of the protein or may be present in a context that is not compatible with integrin binding. Since not all RGD- containing proteins are involved in cell attachment, several other criteria were used to refine the list of RGD- containing proteins. A list of ORFs in the *Chlamydia pneumoniae* genome encoding polypeptides with RGD recognition sequence(s) is in the specification.

Non-*Chlamydia trachomatis* ORFs

Chlamydia pneumoniae ORFs were compared to the ORFs in the *Chlamydia trachomatis* genome (French patent applications FR97-15041, filed 28 November 1997 and 97-16034 filed 17 December 1997) using Blastp. Any *Chlamydia pneumoniae* ORF with a Blastp P value worse than e⁻

[10] (i.e. >e[-10]) against *Chlamydia trachomatis* ORFs are included in this section. A list of ORFs in the *Chlamydia pneumoniae* genome which are not found in *Chlamydia trachomatis* is set forth above in the specification.

5   Cell Wall Anchor Surface ORFs

Many surface proteins are anchored to the cell wall of Gram-positive bacteria via the conserved LPXTG motif (Schneewind, O., Fowler, A., and Faull, K.F. 1995. Structure of the Cell Wall Anchor of Surface Proteins in *Staphylococcus aureus*. Science 268:103-106). A search of the *Chlamydia pneumoniae* ORFs was done using the motif LPXTG. A list of ORFs in the *Chlamydia*
10 *pneumoniae* genome encoding polypeptides anchored to the cell wall is in the specification.

ATCC Deposits

Samples of *Chlamydia pneumoniae* were deposited with the American Type Culture Collection (ATCC), Rockville, Maryland, on November 19, 1998 and assigned the accession
15 · number ---. Cells can be grown, harvested and purified, and DNA can be prepared as discussed above. In order to enable recovery of specific fragments of the chromosome, one can run targeted PCR reactions, whose amplification products can then be sequenced and/or cloned into any suitable vector, according to standard procedures known to those skilled in the art.

In addition, a sample of three pools of clones covering chromosomal regions of interest
20 were deposited with the American Type Culture Collection (ATCC), Rockville, Maryland, on November 19, 1998 and assigned the indicated accession number: — . Each pool of clones contains a series of clones. When taken together, the three pools in the sample cover a portion of the chromosome, with a redundancy of slightly more than two. The total number of clones in the sample is 196.

25   The clones cover the following three regions of interest:
        (i) position 30,000 to 40,000 of SEQ ID No. 1, referred to as region A;
        (ii) position 501,500 to 557,000 of SEQ ID No. 1, referred to as region B; and
        (iii) position 815,000 to 830,000 of SEQ ID No. 1, referred to as region C.

Table 4 lists groups of oligonucleotides to be used to amplify each of ORFs 2-1291
30 according to standard procedures known to those skilled in the art. Such oligonucleotides are listed as SEQ ID Nos. 1292 to 6451. For each ORF, the following is listed: one forward primer positioned 2,000 bp upstream of the beginning of the ORF; one forward primer positioned 200 bp upstream of the beginning of the ORF; one reverse primer positioned 2,000 bp downstream at the end of ORF, which is 2,000 bp upstream of the end site of the ORF on the complementary strand;
35 and one reverse primer 200 bp downstream at the end of ORF, which is 200 bp upstream of the end site of the ORF on the complementary strand. The corresponding SEQ ID Nos. for the primers are listed in Table 4, where Fp is the proximal forward primer; Fd is the distal forward

primer; Bp is the proximal reverse primer; and Bd is the distal reverse primer. The positions of the 5' ends of each of these primers on the nucleotide sequence of SEQ ID No. 1 are shown in Table 5. .

Table 6 lists oligonucleotides (SEQ ID Nos. 6452-6843) to be used to amplify the inserts of each of the 196 clones present in the pooled sample according to standard procedures well known to those of skill in the art. These primers can also be utilized to amplify the chromosomal region corresponding to the region A, B or C within which the particular insert lies. Their positions are indicated in Table 7.

The present invention is not to be limited in scope by the specific embodiments described herein, which are intended as single illustrations of individual aspects of the invention, and functionally equivalent methods and components are within the scope of the invention. Indeed, various modifications of the invention, in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

All publications and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

TABLE 1

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF2	42	794	triosephosphate isomerase	L27492	Thermotoga maritima	567	54
ORF3	1258	1614	putative				
ORF4	1807	2418	polypeptide deformylase	D90906	Synechocystis sp.	316	40
ORF5	3393	2491	hypothetical protein	Z75208	Bacillus subtilis	338	42
ORF6	3639	4067	unknown	U87792	Bacillus subtilis	117	38
ORF7	5649	4270	putative				
ORF8	7463	6012	putative				
ORF9	8051	8962	putative				
ORF10	9129	9959	putative				
ORF11	10687	10361	putative				
ORF12	10927	11232	putative				
ORF13	11246	12727	amidase	U49269	Moraxella catarrhalis	1108	42
ORF14	12691	14190	PET112	D90913	Synechocystis sp.	1044	46
ORF15	14484	17249	POMP91A	U65942	Chlamydia psittaci	1074	43
ORF16	16039	15770	putative				
ORF17	17845	20853	putative				
ORF18	21137	22042	putative				
ORF19	22046	23476	putative				
ORF20	23681	26110	putative				
ORF21	26109	25861	putative				
ORF22	26241	26978	putative				
ORF23	26960	27754	putative				
ORF24	27747	28577	putative				
ORF25	28887	29492	POMP91A	U65942	Chlamydia psittaci	180	39
ORF26	29432	30028	POMP91A	U65942	Chlamydia psittaci	361	51
ORF27	30024	31472	POMP91A	U65942	Chlamydia psittaci	879	54
ORF28	31758	32288	putative 98 kDa outer membrane protein	U72499	Chlamydia psittaci	144	43
ORF29	32201	33991	putative 98 kDa outer membrane protein	U72499	Chlamydia psittaci	1126	48
ORF30	33852	34541	putative 98 kDa outer membrane protein	U72499	Chlamydia psittaci	589	62
ORF31	34783	36063	POMP91B precursor	U65943	Chlamydia psittaci	469	46
ORF32	36009	37529	putative 98 kDa outer membrane protein	U72499	Chlamydia psittaci	1338	51
ORF33	37881	39362	putative 98 kDa outer membrane protein	U72499	Chlamydia psittaci	671	40

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF34	39418	39161	putative				
ORF35	39366	40715	POMP90A precursor	U65942	Chlamydia psittaci	904	47
ORF36	43076	41094	putative				
ORF37	43800	43066	putative				
ORF38	44828	43785	putative				
ORF39	45340	44753	homologous to unidentified E. coli protein	M96343	Bacillus subtilis	136	44
ORF40	45752	45372	o530; This 530 aa orf is 33 pct identical (14 gaps) to 525 residues of an approx. 640 aa protein YHES HAEIN SW: P44808	AE000184	Escherichia coli	269	43
ORF41	46996	45701	ABC transporter, ATP-binding protein (yheS)	AE000596	Helicobacter pylori	878	39
ORF42	47961	47569	putative				
ORF43	48960	48040	hypothetical protein	D64001	Synechocystis sp.	404	37
ORF44	51452	50133	Lon protease-like protein	X74215	Homo sapiens	1232	54
ORF45	52606	51335	unknown	Z54285	Schizosaccharomyces pombe	781	47
ORF46	53684	53319	putative				
ORF47	54195	53746	putative				
ORF48	55278	56453	heat-shock protein	U15010	Legionella pneumophila	975	45
ORF49	56493	57266	branched chain alpha-keto acid dehydrogenase E1-alpha	M97391	Bacillus subtilis	329	36
ORF50	57297	58526	branched chain alpha-keto acid dehydrogenase E1-beta	M97391	Bacillus subtilis	707	50
ORF51	59851	58565	putative				
ORF52	61495	59924	ComE	D90903	Synechocystis sp.	134	55
ORF53	61324	62151	putative				
ORF54	62132	62470	Hpr protein	X12832	Bacillus subtilis	136	36
ORF55	62474	63733	enzyme I (ptsI)	U32844	Haemophilus influenzae	381	35
ORF56	63881	64186	f831; This 831 aa orf is 46 pct identical (11 gaps) to 709 residues of an approx. 712 aa protein PT1A ECOLI SW: P32670	AE000326	Escherichia coli	123	34
ORF57	64611	64318	ORF107	X17014	Bacillus subtilis	128	33
ORF58	65485	64673	putative				
ORF59	65999	65301	dnaZX-like ORF put. DNA polymerase III	X06803	Bacillus subtilis	596	52

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF60	66244	67281	putative				
ORF61	67265	67699	putative				
ORF62	67703	68539	putative				
ORF63	68805	70736	putative				
ORF64	69172	68831	putative				
ORF65	70642	71142	putative				
ORF66	71325	72029	putative				
ORF67	72060	73637	putative				
ORF68	74061	76175	YqfF	D84432	Bacillus subtilis	542	44
ORF69	78351	77680	porphobilinogen deaminase	D28503	Clostridium josui	262	42
ORF70	79356	78355	sms protein	D90914	Synechocystis sp.	736	52
ORF71	79983	79693	ribonuclease III (rnc)	AE000579	Helicobacter pylori	98	33
ORF72	80441	79938	ORF3	D64116	Bacillus subtilis	268	44
ORF73	80475	80969	putative				
ORF74	81296	83080	hypothetical protein	Y14079	Bacillus subtilis	893	38
ORF75	83291	83932	manganese superoxide dismutase	X77021	Caenorhabditis elegans	622	58
ORF76	84005	84769	acetyl-CoA carboxylase beta subunit (accD)	AE000604	Helicobacter pylori	602	50
ORF77	84975	85244	deoxyuridinetriphosphatase (dut)	U32776	Haemophilus influenzae	110	41
ORF78	85123	85425	deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)	AE000596	Helicobacter pylori	265	68
ORF79	85397	85903	ORF2	L26916	Pseudomonas aeruginosa	173	34
ORF80	85909	86583	enzyme IIANtr	U18997	Escherichia coli	170	42
ORF81	86626	88065	putative				
ORF82	89257	91026	putative				
ORF83	91291	93030	putative				
ORF84	93295	94086	putative				
ORF85	95285	94707	putative				
ORF86	95667	96557	putative				
ORF87	96317	97456	putative				
ORF88	98435	97968	putative				
ORF89	99460	98426	putative				
ORF90	100144	101325	elongation factor Tu	L22216	Chlamydia trachomatis	1917	95

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF91	101457	101720	putative				49
ORF92	101704	102273	transcription factor	L10348	Thermus aquaticus thermophilus	376	49
ORF93	102356	102805	ribosomal protein L11	D13303	Bacillus subtilis	458	63
ORF94	102835	103530	ribosomal protein L1	Z11839	Thermotoga maritima	642	51
ORF95	103549	104058	ribosomal protein L10	M89911	Streptomyces antibioticus	82	31
ORF96	104096	104491	rpl12 (AA 1-128)	X53178	Synechocystis PCC6803	325	47
ORF97	104601	108386	DNA-directed RNA polymerase beta chain	X64172	Staphylococcus aureus	2740	52
ORF98	108401	112054	rpoC	V00339	Escherichia coli	2947	54
ORF99	112033	112590	acetylornithine deacetylase (EC 5.1.1.16)	M22622	Leptospira biflexa	514	62
ORF100	112672	113682	transaldolase	L19437	Homo sapiens	755	49
ORF101	113726	114121	putative				
ORF102	114711	114136	putative				
ORF103	115267	115755	putative				
ORF104	115911	116543	putative				
ORF105	116736	118055	ATPase alpha-subunit	X63855	Thermus aquaticus thermophilus	934	50
ORF106	117968	118522	adenosine triphosphatase A subunit	D50528	Acetabularia acetabulum	147	32
ORF107	118530	119843	V-ATPase B subunit	U96487	Desulfurococcus sp. SY	751	48
ORF108	119816	120457	putative				
ORF109	120451	122430	v-type Na-ATPase	X76913	Enterococcus hirae	264	35
ORF110	122504	122950	ATP synthase, subunit K	U67478	Methanococcus jannaschii	184	31
ORF111	123528	126347	valyl-tRNA synthetase	X05891	Escherichia coli	1679	49
ORF112	126332	129166	protein kinase-like protein	U19250	Streptomyces coelicolor	427	37
ORF113	134690	129213	UvrA	D49911	Thermus thermophilus	3107	41
ORF114	134925	136382	pyruvate kinase	U83196	Chlamydia trachomatis	1748	71
ORF115	137870	136482	HtrB protein	X61000	Escherichia coli	147	38
ORF116	137899	138240	putative				
ORF117	138239	137928	putative				
ORF118	139558	138257	putative				
ORF119	140352	139516	YbbP	AB002150	Bacillus subtilis	231	46
ORF120	140498	141841	cyanide insensitive terminal oxidase	Y10528	Pseudomonas aeruginosa	538	50
ORF121	141855	142658	cyanide insensitive terminal oxidase	Y10528	Pseudomonas aeruginosa	310	40
ORF122	144258	143050	putative				
ORF123	145258	144494	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF124	145454	146749	product similar to E. coli PhoH protein	Z97025	Bacillus subtilis	836	47
ORF125	147318	146767	putative				
ORF126	148261	147677	putative				
ORF127	149029	152157	isoleucyl-tRNA synthetase	U04953	Homo sapiens	2361	52
ORF128	154108	152201	leader peptidase I	D90904	Synechocystis sp.	225	47
ORF129	155135	154308	putative				
ORF130	155141	155467	YtiA	AF008220	Bacillus subtilis	201	43
ORF131	155703	156779	orf 361; ranslated orf similarity to SW: RF1_SALTY peptide chain release factor 1 of Salmonella typhimurium	X78969	Coxiella burnetii	863	59
ORF132	156748	157635	product similar to E.coli PRFA2 protein	Z49782	Bacillus subtilis	144	37
ORF133	157653	158996	Ffh	U82109	Thermus aquaticus	797	45
ORF134	159363	159986	tRNA (guanine-N1)-methyltransferase (trmD)	U32705	Haemophilus influenzae	545	49
ORF135	159880	160446	putative				
ORF136	160477	160839	ribosomal protein L19	X72627	Synechocystis sp.	319	50
ORF137	160898	161539	putative protein highly homologous to E. coli RNase HII.	D32253	Magnetospirillum sp.	427	49
ORF138	161527	162153	5'guanylate kinase (gmk)	U32848	Haemophilus influenzae	385	43
ORF139	162144	162443	putative				
ORF140	162437	164098	methionyl-tRNA synthetase	AB004537	Schizosaccharomyces pombe	861	54
ORF141	165451	164228	exodeoxyribonuclease V (recD)	U32811	Haemophilus influenzae	432	32
ORF142	166349	165411	putative				
ORF143	166949	168442	putative				
ORF144	169416	171029	putative				
ORF145	170857	171459	putative				
ORF146	172652	173428	putative biotin-protein ligase	Z97992	Schizosaccharomyces pombe	292	44
ORF147	174626	173439	putative				
ORF148	174816	175613	putative				
ORF149	175598	175954	putative				
ORF150	175958	176935	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF151	177708	176938	orf 3'of chaperonin homolog hypB [Chlamydia psittaci, pigeon strain P-1041, Peptide Partial. 98 aa]	S40172	Chlamydia psittaci	376	74
ORF152	177128	177376	putative				
ORF153	179472	177841	putative	M69217	Chlamydia pneumoniae	2678	100
ORF154	179822	179517	putative	M69217	Chlamydia pneumoniae	498	99
ORF155	181793	179943	Pz-peptidase	D88209	Bacillus licheniformis	1088	38
ORF156	182628	181876	o247; This 247 aa orf is 51 pct identical (0 gaps) to 117 residues of an approx. 160 aa protein YPH7 CHRVI SW: P45371	AE000174	Escherichia coli	401	42
ORF157	184420	183074	glutamate-1-semialdehyde 2,1-aminomutase	X53696	Escherichia coli	823	41
ORF158	184988	184467	ORF o211	U28377	Escherichia coli	87	54
ORF159	185483	185112	hypothetical protein	D90906	Synechocystis sp.	91	33
ORF160	185902	185483	ribose 5-phosphate isomerase	U28377	Escherichia coli	111	41
ORF161	186174	185839	ribose 5-phosphate isomerase A (SP:P27252)	U32729	Haemophilus influenzae	190	46
ORF162	187720	186587	hypothetical	D83026	Bacillus subtilis	536	42
ORF163	188318	190933	ATP-dependent protease binding subunit	M29364	Escherichia coli	2010	53
ORF164	191090	191635	putative				
ORF165	191547	192743	putative				
ORF166	192969	193469	putative				
ORF167	194044	193610	putative				
ORF168	194196	195809	unknown	Z84395	Mycobacterium tuberculosis	242	52
ORF169	196088	198073	DNA ligase (EC 6.5.1.2)	M24278	Escherichia coli	1317	46
ORF170	198132	199454	putative				
ORF171	199351	202818	putative				
ORF172	204552	202999	PcpB	U60175	Sphingomonas chlorophenolica	80	41
ORF173	205648	204692	putative				
ORF174	205807	207327	leucine tRNA synthetase	AF008220	Bacillus subtilis	1595	57
ORF175	207182	207775	leucyl-tRNA synthetase	X06331	Escherichia coli	363	51
ORF176	207779	208267	transfer RNA-Leu synthetase	M88581	Bacillus subtilis	285	43
ORF177	208267	209577	KDO transferase	Z31593	Chlamydia pneumoniae	2262	100

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF178	211807	211271	KDO-transferase	X80061	Chlamydia psittaci	105	38
ORF179	212188	211844	putative				
ORF180	214079	212448	pyrophosphate-dependent phosphofructokinase beta subunit	Z32850	Ricinus communis	1003	45
ORF181	214907	214083	CinI	U44893	Butyrivibrio fibrisolvens	111	41
ORF182	216154	215429	putative				
ORF183	216115	216678	putative				
ORF184	216728	217282	putative				
ORF185	217267	217866	putative				
ORF186	218593	218261	putative				
ORF187	219821	218994	putative				
ORF188	221382	220309	putative				
ORF189	222719	221433	GMP synthetase	M10101	Escherichia coli	1151	48
ORF190	223521	222724	IMP dehydrogenase	X66859	Acinetobacter calcoaceticus	778	58
ORF191	224499	225008	putative				
ORF192	225140	225559	putative				
ORF193	225555	226802	putative				
ORF194	227800	226892	putative				
ORF195	228335	228072	putative				
ORF196	229251	228643	putative				
ORF197	230983	229622	YqhX	D84432	Bacillus subtilis	1386	56
ORF198	231483	230983	acetyl-CoA carboxylase biotin carboxyl carrier protein	U38804	Porphyra purpurea	199	52
ORF199	232063	231509	elongation factor P	D64001	Synechocystis sp.	282	32
ORF200	232739	232053	pentose-5-phosphate-3-epimerase	D90911	Synechocystis sp.	463	43
ORF201	233166	234356	putative				
ORF202	233518	233165	putative				
ORF203	234536	235186	ORF2	L35036	Chlamydia psittaci	570	60
ORF204	235379	236689	putative				
ORF205	236680	237618	putative				
ORF206	237521	238345	putative				
ORF207	238281	238973	putative				
ORF208	238871	240115	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF209	240191	241564	putative				
ORF210	242281	241604	YqiZ	D84432	Bacillus subtilis	379	39
ORF211	242933	242274	f222; This 222 aa orf is 48 pct identical (0 gaps) to 208 residues of an approx. 232 aa protein YCKA BACSU SW: P42399	AE000284	Escherichia coli	382	45
ORF212	243416	242976	arginine repressor protein (argR)	U32800	Haemophilus influenzae	229	46
ORF213	243500	244531	sialoglycoprotease	U15958	Pasteurella haemolytica	565	53
ORF214	244480	246021	oligopeptide permease homolog AII	AF000366	Borrelia burgdorferi	457	34
ORF215	246330	247811	OppAIV	AF000948	Borrelia burgdorferi	453	35
ORF216	247831	249174	OppA gene product	X56347	Bacillus subtilis	255	37
ORF217	249437	251038	dciAE	X56678	Bacillus subtilis	469	37
ORF218	251325	252212	OppB gene product	X56347	Bacillus subtilis	652	42
ORF219	253156	254007	oligopeptidepermease	X89237	Streptococcus pyogenes	574	48
ORF220	253974	254852	ATP binding protein	L18760	Lactococcus lactis	433	40
ORF221	255258	256094	KDO-transferase	X80061	Chlamydia psittaci	106	46
ORF222	256640	257455	putative				
ORF223	257502	258239	2-OXOGLUTARAT	A47930	Spinacia oleracea	636	52
ORF224	257869	257501	putative				
ORF225	259248	260897	pyrophosphate-fructose 6-phosphate 1-phosphotransferase beta-subunit	M55191	Solanum tuberosum	1055	44
ORF226	262753	261788	putative				
ORF227	263059	262757	putative				
ORF228	264375	263182	putative				
ORF229	265985	264747	putative				
ORF230	266637	266059	putative				
ORF231	267338	266538	putative				
ORF232	267922	267473	putative				
ORF233	269647	270771	tRNA guanine transglycosylase	L33777	Zymomonas mobilis	628	44
ORF234	272777	273145	ORF 4	D00624	Bacteriophage chp1	100	41
ORF235	273253	273636	putative				
ORF236	273705	273977	putative				
ORF237	276016	275717	putative				
ORF238	276439	276020	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF239	276792	277253	putative				
ORF240	277318	277599	putative				
ORF241	278578	277877	putative				
ORF242	279258	278554	FbpC	U33937	Neisseria gonorrhoeae	312	39
ORF243	280435	279533	putative				
ORF244	281547	280849	putative				
ORF245	281696	282325	CMP-2-keto-3-deoxyoctulosonic acid synthetase	U15192	Chlamydia trachomatis	637	63
ORF246	282459	284069	CTP synthetase	U15192	Chlamydia trachomatis	2000	68
ORF247	284056	284517	ORF3	U15192	Chlamydia trachomatis	453	65
ORF248	284606	285775	glucose 6-phosphate dehydrogenase	U83195	Chlamydia trachomatis	1263	77
ORF249	285592	285987	glucose 6-phosphate dehydrogenase	U83195	Chlamydia trachomatis	519	79
ORF250	286179	286976	glucose-6-phosphate dehydrogenase isozyme	D88189	Actinobacillus actinomycetemcomitans	216	40
ORF251	287583	287002	putative				
ORF252	287951	287451	putative				
ORF253	288499	288816	putative				
ORF254	289674	288505	putative				
ORF255	288839	289213	putative				
ORF256	289970	290254	putative				
ORF257	291931	292803	gamma-D-glutamyl-L-diamino acid endopeptidase II	X64809	Bacillus sphaericus	95	39
ORF258	293258	292755	ScoS9	U43429	Streptomyces coelicolor	233	45
ORF259	293718	293272	ribosomal protein L13 (rpL13)	U32823	Haemophilus influenzae	364	47
ORF260	294630	293953	glutamine transport ATP-binding protein Q	U67524	Methanococcus jannaschii	387	46
ORF261	296153	294636	putative				
ORF262	294817	295068	putative				
ORF263	296354	297862	conserved hypothetical protein	AE000586	Helicobacter pylori	641	46
ORF264	298415	297879	putative				
ORF265	298777	298253	putative				
ORF266	299572	298781	putative				
ORF267	300487	299633	putative				
ORF268	301586	300702	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF269	302440	301571	putative				
ORF270	302838	302437	putative				
ORF271	303335	302745	putative				
ORF272	304394	303852	putative				
ORF273	304606	305223	f311; This 311 aa orf is 22 pct identical (13 gaps) to 186 residues of an approx. 488 aa protein YACA_BACSU SW: P37563; pyuI of D21139	AE000232	Escherichia coli	250	38
ORF274	305394	306236	survival protein surE	U81296	Sinorhizobium meliloti	156	42
ORF275	306501	307439	YqfU	D84432	Bacillus subtilis	547	42
ORF276	308033	307458	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	U61168	Bacillus firmus	403	42
ORF277	308924	308037	4-hydroxybenzoate octaprenyltransferase	U61168	Bacillus firmus	152	40
ORF278	309485	310180	putative				
ORF279	310426	311214	putative				
ORF280	311597	311253	putative				
ORF281	312772	311780	putative				
ORF282	313425	312772	putative				
ORF283	313646	313377	putative				
ORF284	313937	314665	lysophospholipase homolog	AF006678	Schistosoma mansoni	141	44
ORF285	315576	314755	dnaZX	X17014	Bacillus subtilis	154	39
ORF286	316157	315531	unknown	D26185	Bacillus subtilis	284	31
ORF287	318657	316156	DNA gyrase	L47978	Aeromonas salmonicida	1785	48
ORF288	321042	318676	DNA gyrase subunit B	U35453	Clostridium acetobutylicum	1838	59
ORF289	321445	321098	putative				
ORF290	322309	321710	putative				
ORF291	323190	322366	outer membrane protein	AE000654	Helicobacter pylori	376	43
ORF292	323843	323181	hypothetical	U70214	Escherichia coli	356	37
ORF293	324878	323856	ATP-binding protein (abc)	U32744	Haemophilus influenzae	545	44
ORF294	325340	326410	f374; This 374 aa orf is 30 pct identical (9 gaps) to 102 residues of an approx. 512 aa protein FLIC_SALMU SW: P06177	AE000299	Escherichia coli	1194	62
ORF295	326433	327836	Xas A	AE000246	Escherichia coli	479	33

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF296	328465	327839	putative				
ORF297	329360	328857	putative				
ORF298	330907	329357	putative				
ORF299	332455	330956	MgtE	U18744	Bacillus firmus	203	36
ORF300	334536	332395	putative				
ORF301	336091	334877	putative				
ORF302	336103	337302	putative				
ORF303	338129	338830	putative				
ORF304	338965	339501	putative				
ORF305	339508	340143	putative				
ORF306	340247	342967	putative				
ORF307	343385	343810	cAMP-dependent protein kinase type I regulatory subunit	U75932	Rattus norvegicus	102	37
ORF308	344171	343935	acyl carrier protein (acpP)	AE000570	Helicobacter pylori	198	55
ORF309	345082	344330	3-ketoacyl-ACP reductase	U39441	Vibrio harveyi	598	48
ORF310	346005	345082	malonyl-CoA:Acyl carrier protein transacylase	U59433	Bacillus subtilis	538	45
ORF311	346784	346437	beta-ketoacyl-acyl carrier protein synthase III (fabH)	AE000540	Helicobacter pylori	273	50
ORF312	347029	346715	beta-ketoacyl-acyl carrier protein synthase III	M77744	Escherichia coli	265	63
ORF313	347034	347723	recombination protein	D90916	Synechocystis sp.	363	42
ORF314	348075	350459	putative				
ORF315	350598	351071	putative				
ORF316	351075	352175	rifampicin resistance protein	L22690	Rickettsia rickettsii	495	46
ORF317	353291	352230	putative				
ORF318	353442	354467	pyruvate dehydrogenase E1 component, alpha subunit	D90915	Synechocystis sp.	571	44
ORF319	354451	354933	pyruvate dehydrogenase E1 beta subunit	U09137	Arabidopsis thaliana	495	59
ORF320	355000	355449	pyruvate dehydrogenase E1 component, beta subunit	U38804	Porphyra purpurea	336	47
ORF321	355448	356743	F23B12.5	Z77659	Caenorhabditis elegans	759	46
ORF322	355953	355642	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF323	359310	356827	glycogen phosphorylase B	U47025	Homo sapiens	2193	57
ORF324	359120	359377	putative				
ORF325	359525	359908	putative				
ORF326	361290	359947	DnaA	D89066	Staphylococcus aureus	375	46
ORF327	363785	361362	hypothetical	U32781	Haemophilus influenzae	394	44
ORF328	364496	363888	putative				
ORF329	364832	365290	putative				
ORF330	365304	365669	dpi	M76470	Escherichia coli	160	45
ORF331	366599	365667	NADPH thioredoxin reductase	AC002329	Arabidopsis thaliana	975	60
ORF332	367291	369030	ribosomal protein S1 (rpS1)	U32801	Haemophilus influenzae	1209	41
ORF333	369134	369808	NusA	U74759	Chlamydia trachomatis	995	87
ORF334	369917	370438	NusA	U74759	Chlamydia trachomatis	760	87
ORF335	370365	372647		U74759	Chlamydia trachomatis	2173	61
ORF336	372557	373066	initiation factor IF2-beta (infB; gtg start codon)	X00513	Escherichia coli	333	39
ORF337	373020	373442	ORF6 gene product	Z18631	Bacillus subtilis	192	34
ORF338	373467	374195	tRNA pseudouridine 55 synthase	D90917	Synechocystis sp.	358	47
ORF339	374176	375099	hypothetical 34.6 kD protein in rpsT-ileS intergenic region	AE000113	Escherichia coli	395	39
ORF340	375676	375083	hypothetical GTP-binding protein in pth 3' region	AE000219	Escherichia coli	507	53
ORF341	376173	375634	hypothetical	U32723	Haemophilus influenzae	480	59
ORF342	376564	377643	YscU	U08019	Yersinia enterocolitica	538	37
ORF343	377956	379773	lcrD gene product	X67771	Yersinia enterocolitica	1302	47
ORF344	379781	380425	putative				
ORF345	380281	381000	putative				
ORF346	381008	381460	putative				
ORF347	381460	383037	4-alpha-glucanotransferase	L37874	Clostridium butyricum	302	38
ORF348	383257	383523	ribosomal protein L28 (rpL28)	U32776	Haemophilus influenzae	175	55
ORF349	383553	385304	hypothetical protein	D90901	Synechocystis sp.	565	38
ORF350	385397	386458	comE ORF1	D64002	Synechocystis sp.	187	10
ORF351	387242	386514	putative				
ORF352	388764	387013	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF353	390120	390932	methylenetetrahydrofolate dehydrogenase	D64000	Synechocystis sp.	588	53
ORF354	390919	391818	f351; Residues 1-121 are 100 pct identical to YOIL_ECOLI SW: P33944 (122 aa) and aa 152-351 are 100 pct identical to YOIK_ECOLI SW: P33943	AE000310	Escherichia coli	186	39
ORF355	392379	391885	small protein	D90914	Synechocystis sp.	387	46
ORF356	392582	392986	putative				
ORF357	392776	393684	putative				
ORF358	394151	394804	RecF protein	D90907	Synechocystis sp.	232	34
ORF359	394928	395308	putative				
ORF360	395259	395990	putative				
ORF361	397815	395953	hypothetical	U32773	Haemophilus influenzae	391	36
ORF362	398850	397831	H. influenzae predicted coding region HI0807	U32763	Haemophilus influenzae	580	39
ORF363	400085	399099	putative				
ORF364	401245	400073	YtgC	AF008220	Bacillus subtilis	244	30
ORF365	401474	401136	putative				
ORF366	402199	401423	unknown	U52850	Erysipelothrix rhusiopathiae	534	46
ORF367	403193	402186	putative				
ORF368	403650	404165	putative				
ORF369	404343	405914	adenine nucleotide translocase	Z49227	Arabidopsis thaliana	1280	55
ORF370	405984	407327	putative				
ORF371	407712	408806	putative				
ORF372	410439	409075	putative				
ORF373	411826	410954	putative				
ORF374	412482	414302	lepA gene product	X91655	Bacillus subtilis	1827	59
ORF375	415402	414407	6-phosphogluconate dehydrogenase, decarboxylating (gnd)	U32737	Haemophilus influenzae	687	51
ORF376	415848	415237	6-phosphogluconate dehydrogenase, 6PGD [Ceratitis capitata=medflies, Peptide, 481 aa]	S67873	Ceratitis capitata	695	64
ORF377	417131	415866	tyrosyl-tRNA synthetase (tyrS)	J01719	Escherichia coli	821	45
ORF378	417258	417566	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF379	418326	417454	whiG-Stv gene product	X68709	*Streptoverticillium griseocarneum*	464	41
ORF380	420057	418426	FLHA gene product	X63698	*Bacillus subtilis*	455	49
ORF381	420448	420720	ferredoxin IV	M59855	*Rhodobacter capsulatus*	174	63
ORF382	420980	421552	putative				
ORF383	421556	422029	putative				
ORF384	422461	422925	putative				
ORF385	423562	424320	putative				
ORF386	424250	424591	putative				
ORF387	424830	426047	putative				
ORF388	426240	427397	putative				
ORF389	428841	430703	GcpE	D90908	*Synechocystis sp.*	877	47
ORF390	430694	431446	YfiH	U50134	*Escherichia coli*	136	35
ORF391	431597	432100	putative				
ORF392	432165	432779	putative				
ORF393	433272	432832	dihydrolipoamide succinyltransferase (sucB)	U32839	*Haemophilus influenzae*	475	64
ORF394	433925	433227	dihydrolipoamide succinyltransferase (sucB)	U32839	*Haemophilus influenzae*	332	45
ORF395	436678	433934	alpha-ketoglutarate dehydrogenase	U41762	*Rhodobacter capsulatus*	1530	44
ORF396	437176	438357	oxygen-independent coproporphyrinogen III oxidase (hemN)	AE000628	*Helicobacter pylori*	442	42
ORF397	440317	438518	putative				
ORF398	440001	440345	putative				
ORF399	441233	440517	ORF f286	U18997	*Escherichia coli*	168	45
ORF400	440719	441012	putative				
ORF401	442192	441230	putative				
ORF402	442888	442343	putative				
ORF403	442371	442961	putative				
ORF404	443578	443003	[karp] gene products	M86605	*Chlamydia trachomatis*	505	78
ORF405	444500	443526	aminopeptidase	D17450	*Mycoplasma salivarium*	273	39
ORF406	444842	444528	putative				
ORF407	445009	444743	putative	L39923	*Mycobacterium leprae*	133	33

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF408	445718	445182	putative				
ORF409	445807	447804	Sulp	U18908	Zea mays	1307	52
ORF410	448738	447803	putative				
ORF411	449628	448618	RuvB protein	U38840	Thermotoga maritima	845	53
ORF412	450298	450867	deoxycytidine triphosphate deaminase (dcd)	AE000554	Helicobacter pylori	573	58
ORF413	450713	451207	putative				
ORF414	451211	452452	hemolysin	D90914	Synechocystis sp.	227	39
ORF415	452448	453659	similar to [SwissProt Accession Number P37908]	D90888	Escherichia coli	96	33
ORF416	454843	453725	NifS gene product	L34879	Anabaena azollae	533	38
ORF417	455608	454865	hypothetical protein	D90908	Synechocystis sp.	371	36
ORF418	456243	457007	putative				
ORF419	457016	457708	putative				
ORF420	458368	457979	unknown	D26185	Bacillus subtilis	152	36
ORF421	459496	458372	mutY homolog	U63329	Homo sapiens	466	46
ORF422	459493	460194	hypothetical protein	D90914	Synechocystis sp.	98	38
ORF423	461446	460355	putative				
ORF424	462298	461450	putative				
ORF425	462444	463349	enoyl-ACP reductase	Y13861	Nicotiana tabacum	1008	69
ORF426	464241	463342	putative				
ORF427	464574	465065	putative				
ORF428	465129	465611	putative				
ORF429	465571	466317	putative				
ORF430	466317	467093	H. pylori predicted coding region HP0152	AE000536	Helicobacter pylori	246	36
ORF431	466999	467502	putative				
ORF432	469691	467715	unidentified transporter-ATP binding	Z82044	Bacillus subtilis	496	45
ORF433	470691	469660	acetyl-CoA carboxylase subunit	AF008220	Bacillus subtilis	781	52
ORF434	472010	470709	putative				
ORF435	471545	471799	putative				
ORF436	472359	472045	putative				
ORF437	473523	472732	orf1	X75413	Escherichia coli	313	42
ORF438	474889	473441	murE gene product	Z15056	Bacillus subtilis	679	37
ORF439	477323	475365	penicillin-binding protein 2	X59630	Neisseria meningitidis	451	42

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF440	478496	477597	hypothetical protein	D90906	Synechocystis sp.	534	52
ORF441	478722	479273	putative				
ORF442	479277	479705	putative				
ORF443	480050	481450	chromosomal replication initiator protein DnaA	D90909	Synechocystis sp.	793	40
ORF444	481469	482053	OrfH	U35673	Borrelia burgdorferi	157	37
ORF445	482600	482025	putative				
ORF446	482654	484204	NADH:ubiquinone oxidoreductase subunit B	Z37111	Vibrio alginolyticus	801	49
ORF447	484211	485170	NADH:ubiquinone oxidoreductase (GP:Z37111 4)	U32702	Haemophilus influenzae	258	48
ORF448	485170	485838	NADH:uniquinone oxidoreductase	Z37111	Vibrio alginolyticus	543	55
ORF449	485813	486580	unidentified protein of Na+-translocating NADH-quinone reductase	D49364	Vibrio alginolyticus	488	48
ORF450	486976	486638	putative				
ORF451	489071	487764	putative				
ORF452	489341	489090	putative				
ORF453	489958	489152	putative				
ORF454	490549	489962	putative				
ORF455	491163	490522	putative				
ORF456	491396	491112	putative				
ORF457	492121	491390	putative				
ORF458	492304	494838	ClpC adenosine triphosphatase	U02604	Bacillus subtilis	2370	46
ORF459	495943	494822	hypothetical protein in purB 5' region	AE000213	Escherichia coli	927	53
ORF460	496011	496565	putative				
ORF461	496569	497228	putative				
ORF462	497358	497834	putative				
ORF463	497770	498327	putative				
ORF464	499209	499589	putative				
ORF465	499520	499792	putative				
ORF466	500774	504169	putative 98 kDa outer membrane protein	U72499	Chlamydia psittaci	1215	45
ORF467	504139	504600	putative 98 kDa outer membrane protein	U72499	Chlamydia psittaci	319	47
ORF468	504865	506877	putative 98 kDa outer membrane protein	U72499	Chlamydia psittaci	992	42

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF469	506790	507671	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	739	46
ORF470	507718	510507	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	1813	42
ORF471	508325	507912	putative				
ORF472	510660	513440	POMP90A precursor	U65942	*Chlamydia psittaci*	1830	46
ORF473	514965	513787	hypothetical	D83026	*Bacillus subtilis*	482	48
ORF474	517347	515419	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	1554	51
ORF475	517058	517363	putative				
ORF476	517798	517277	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	222	41
ORF477	518200	517847	POMP91B precursor	U65943	*Chlamydia psittaci*	162	42
ORF478	518300	521146	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	1900	45
ORF479	521392	522948	POMP91A	U65942	*Chlamydia psittaci*	490	39
ORF480	523244	524809	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	507	35
ORF481	524379	524125	putative				
ORF482	524649	526238	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	969	41
ORF483	526265	527104	putative				
ORF484	526947	526702	putative				
ORF485	526975	528450	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	197	48
ORF486	528408	529199	putative outer membrane protein	U72499	*Chlamydia psittaci*	154	37
ORF487	530612	529542	putative				
ORF488	531656	530616	putative				
ORF489	533974	532067	putative				
ORF490	536432	534324	putative				
ORF491	537150	536707	putative				
ORF492	537928	537080	putative				
ORF493	538438	537932	putative				
ORF494	538737	538333	putative				
ORF495	539594	539127	putative				
ORF496	541215	539590	putative				
ORF497	542571	541282	putative				
ORF498	543014	542457	putative				
ORF499	543369	542962	putative				
ORF500	543809	546628	putative 98 kDa outer membrane protein	U72499	*Chlamydia psittaci*	506	89
ORF501	546619	549525	POMP91A	U65942	*Chlamydia psittaci*	128	50

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF502	547293	546994	putative				
ORF503	549699	550523	putative 98 kDa outer membrane protein	U72499	Chlamydia psittaci	96	32
ORF504	550490	551551	putative 98 kDa outer membrane protein	U72499	Chlamydia psittaci	223	33
ORF505	551448	552623	putative 98 kDa outer membrane protein	U72499	Chlamydia psittaci	139	46
ORF506	552652	555117	putative 98 kDa outer membrane protein	U72499	Chlamydia psittaci	487	48
ORF507	555029	555493	putative				
ORF508	558006	555673	putative				
ORF509	559694	558162	putative				
ORF510	558208	558573	putative				
ORF511	561692	559899	putative				
ORF512	561412	561708	putative				
ORF513	563942	561777	1,4-alpha-glucan branching enzyme	X73903	Streptomyces coelicolor	1743	45
ORF514	564969	563950	putative				
ORF515	566204	564936	YqeV	D84432	Bacillus subtilis	639	38
ORF516	567717	566302	putative GTPase required for high frequency lysogenization by bacteriophage lambda	U00005	Escherichia coli	686	41
ORF517	568526	567708	putative				
ORF518	569467	568742	putative				
ORF519	571065	569431	putative				
ORF520	571828	571118	arginine-binding periplasmic protein 1 precursor	AE000188	Escherichia coli	197	45
ORF521	572202	573308	putative				
ORF522	573146	575056	putative				
ORF523	575023	575916	carboxysome formation protein	D90901	Synechocystis sp.	557	59
ORF524	577891	576497	putative				
ORF525	578914	578204	putative				
ORF526	579924	578857	putative				
ORF527	580187	579858	protein kinase C inhibitor	D90906	Synechocystis sp.	260	49
ORF528	580017	580406	putative				
ORF529	581086	580187	Yer156cp	U18917	Saccharomyces cerevisiae	176	34
ORF530	581367	581828	putative				
ORF531	581678	582367	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF532	582361	583428	putative				
ORF533	584690	583431	putative				
ORF534	585237	584950	putative				
ORF535	585626	586888	hypothetical protein	D64004	Synechocystis sp.	805	45
ORF536	586846	587907	putative				
ORF537	589049	588180	putative				
ORF538	590500	589301	putative				
ORF539	590755	592458	aminoacyl-tRNA synthetase	L25105	Chlamydia trachomatis	2125	71
ORF540	592526	592903	has homology to putative heat shock proteins of Bacillus subtilis and Clostridium acetobutylicum: ORFA: putative	L25105	Chlamydia trachomatis	324	59
ORF541	592836	593747	Possible negative regulator of CIRCE element; Homologs in B. subtilis and Clostridia spp. referred to as hrcA or orfA	U52216	Chlamydia trachomatis	960	65
ORF542	593747	594298	grpE	M62819	Chlamydia trachomatis	661	71
ORF543	594331	595947	DnaK protein homolog; 71,550 Da; putative	M69227	Chlamydia pneumoniae	2619	100
ORF544	595905	596309	DnaK protein homolog; 71,550 Da; putative	M69227	Chlamydia pneumoniae	674	100
ORF545	596514	597215	putative				
ORF546	597184	597957	vacB gene product	U14003	Escherichia coli	306	48
ORF547	597755	598612	ORF-2	D11024	Shigella flexneri	168	46
ORF548	598602	599204	homologous to DNA glycosylases; hypothetical	D83026	Bacillus subtilis	374	47
ORF549	599373	599939	putative				
ORF550	600903	602072	hemolysin	X73141	Serpulina hyodysenteriae	362	36
ORF551	602240	602587	hypothetical protein	D90908	Synechocystis sp.	182	35
ORF552	602637	603272	putative				
ORF553	603142	604512	putative				
ORF554	604627	605853	conserved hypothetical protein	AE000579	Helicobacter pylori	423	40
ORF555	605790	606620	putative				
ORF556	606571	607281	putative	L14679	Lactococcus lactis	384	45
ORF557	609004	607355	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF558	610906	609932	putative				
ORF559	611786	611004	diaminopimelate epimerase	D90917	Synechocystis sp.	207	55
ORF560	612333	611746	ATP-dependent Clp protease proteolytic subunit	D90915	Synechocystis sp.	389	44
ORF561	613897	612341	serine hydroxymethyltransferase	D90903	Synechocystis sp.	909	52
ORF562	615179	616279	putative				
ORF563	616610	617383	putative				
ORF564	618796	617810	ORF o328	U18997	Escherichia coli	413	45
ORF565	620004	618826	branched chain alpha-keto acid dehydrogenase E2	M97391	Bacillus subtilis	688	41
ORF566	619649	619918	putative				
ORF567	621265	620021	Hypothetical protein	Y14083	Bacillus subtilis	727	37
ORF568	622359	621265	hypothetical	U32691	Haemophilus influenzae	294	52
ORF569	623420	622560	rRNA methylase	D90913	Synechocystis sp.	244	38
ORF570	624297	623335	hypothetical protein (SP:P39587)	U67605	Methanococcus jannaschii	147	35
ORF571	624773	624174	riboflavin synthase alpha chain	AE000261	Escherichia coli	424	50
ORF572	625029	625484	ORF 168	D28752	Synechococcus sp.	323	43
ORF573	625488	625883	YteA	AF008220	Bacillus subtilis	172	35
ORF574	625892	626395	signalpeptidase II	X78084	Staphylococcus carnosus	204	38
ORF575	626444	627790	D-alanine permease (dagA)	U32770	Haemophilus influenzae	566	33
ORF576	627912	628607	putative				
ORF577	628774	629697	putative				
ORF578	629660	631639	POMP91A	U65942	Chlamydia psittaci	579	44
ORF579	631725	633551	putative				
ORF580	633520	636957	putative 98 kDa outer membrane protein	U72499	Chlamydia psittaci	266	45
ORF581	637232	638098	adhesion protein	D90903	Synechocystis sp.	267	38
ORF582	640648	639593	GTP-binding protein	D90901	Synechocystis sp.	759	45
ORF583	640979	640728	50S ribosomal protein L27	U38804	Porphyra purpurea	265	65
ORF584	641327	641007	50S ribosomal subunit protein L21	U18997	Escherichia coli	210	41
ORF585	641687	642283	hypothetical protein	D90906	Synechocystis sp.	76	39
ORF586	643023	642286	assimilatory sulfite reductase	L26503	Saccharomyces cerevisiae	284	42
ORF587	643330	643076	putative				
ORF588	643704	643351	ribosomal protein S10 (rpS10)	U32761	Haemophilus influenzae	349	69

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF589	645628	643676	translation elongation factor EF-G (fusA)	AE000625	Helicobacter pylori	1991	58
ORF590	645783	645538	elongation factor G (AA 1-691)	X16278	Thermus aquaticus thermophilus	170	80
ORF591	646269	645793	ribosomal protein S7	Z11567	Chlamydia trachomatis	730	88
ORF592	646751	646314	ribosomal protein S12 (AA 1-123)	X52912	Cryptomonas phi	485	67
ORF593	647848	647045	putative				
ORF594	648393	650336	ORF of prc gene (alt.)	D00674	Escherichia coli	554	42
ORF595	651016	650420	hypothetical sulfur-rich protein	U41759	Chlamydia psittaci	301	50
ORF596	652956	651289	60kDa CrP	X53511	Chlamydia pneumoniae	2951	100
ORF597	653395	653126	9kDa CrP	X53511	Chlamydia pneumoniae	502	99
ORF598	655740	654193	glutamyl-tRNA synthetase homolog	U41759	Chlamydia psittaci	2259	82
ORF599	656508	655966	early stage-specific transcription experimentally demonstrated; early upstream open reading frame (EUO)	L13598	Chlamydia psittaci	666	62
ORF600	658140	657022	unknown	U41759	Chlamydia psittaci	950	44
ORF601	660216	658525	RecJ recombination protein	U41759	Chlamydia psittaci	807	73
ORF602	663238	660248	protein-export membrane protein SecD	D64000	Synechocystis sp.	413	41
ORF603	664461	663157	putative				
ORF604	665735	664635	putative				
ORF605	666212	666994	hypothetical protein	D64006	Synechocystis sp.	538	58
ORF606	666998	667921	o298; This 298 aa orf is 33 pct identical (24 gaps) to 248 residues of an approx. 256 aa protein CDSA_ECOLI SW: P06466	AE000238	Escherichia coli	253	45
ORF607	667909	668568	cytidylate kinase	AE000193	Escherichia coli	400	48
ORF608	668502	669203	hypothetical protein	D90915	Synechocystis sp.	225	33
ORF609	669154	670893	arginyl-tRNA-synthetase	D64006	Synechocystis sp.	1365	49
ORF610	672226	670853	UDP-N-acetylglucosamine enolpyruvyl transferase (murZ)	U32788	Haemophilus influenzae	642	40
ORF611	671137	671424	putative				
ORF612	672453	673001	putative				
ORF613	673072	674721	putative				
ORF614	674549	674262	putative				
ORF615	675518	674796	ORF246 gene product	X59551	Escherichia coli	520	43
ORF616	676083	675499	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF617	676630	676067	putative				
ORF618	677016	676600	ORF3	D10279	Bacillus subtilis	361	63
ORF619	677647	677015	peptide release factor 2	X99401	Bacillus firmus	427	43
ORF620	677990	678259	unknown	Z49939	Saccharomyces cerevisiae	175	48
ORF621	679444	680097	unknown	D26185	Bacillus subtilis	263	38
ORF622	680097	680897	unknown	D64126	Bacillus subtilis	506	45
ORF623	681637	680849	putative				
ORF624	681409	682281	putative				
ORF625	682453	682821	putative				
ORF626	682763	683902	sensor protein	L39904	Myxococcus xanthus	190	48
ORF627	684616	683969	putative				
ORF628	685169	684534	putative				
ORF629	685986	685117	putative				
ORF630	686278	687288	NtrC/NifA-like protein regulator	U17902	Escherichia coli	820	45
ORF631	687483	688151	putative				
ORF632	688740	689501	putative				
ORF633	690242	689622	putative				
ORF634	690470	691126	unknown	Z48008	Saccharomyces cerevisiae	380	46
ORF635	692600	691497	putative				
ORF636	692674	695064	phenylalanyl-tRNA synthetase beta-subunit (pheT)	U32810	Haemophilus influenzae	593	45
ORF637	695049	696032	putative				
ORF638	697964	696585	OppC-like protein	D85103	Synechococcus sp.	371	37
ORF639	699803	698274	OppB gene product	X56347	Bacillus subtilis	197	40
ORF640	701926	699788	AppA	U20909	Bacillus subtilis	324	43
ORF641	703196	702567	putative				
ORF642	704221	703208	putative				
ORF643	704240	705289	ferrochelatase	X73417	Arabidopsis thaliana	266	42
ORF644	706070	705300	histidine periplasmic binding protein P29	U58045	Campylobacter jejuni	128	31
ORF645	706841	706254	conserved hypothetical protein	AE000592	Helicobacter pylori	155	37
ORF646	707596	706811	putative				
ORF647	708666	707677	ADP-glucose pyrophosphorylase	X55650	Solanum tuberosum	595	43
ORF648	709793	709119	pyrE-F gene product	X71842	Arabidopsis thaliana	400	44

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF649	711523	710132	transcription termination factor	J01673	Escherichia coli	1251	60
ORF650	712236	711523	putative				
ORF651	714734	712125	DNA polymerase I	J04479	Streptococcus pneumoniae	1334	43
ORF652	715759	714761	protease IV	U67512	Methanococcus jannaschii	101	55
ORF653	717538	715886	adenine nucleotide translocase	Z49227	Arabidopsis thaliana	832	39
ORF654	719113	720243	replicative DNA helicase	D26185	Bacillus subtilis	776	44
ORF655	720590	722422	homologous to E.coli gidA	X62540	Pseudomonas putida	1575	52
ORF656	722406	723056	putative				
ORF657	723551	723120	nucleoside 5'-diphosphate phosphotransferase (EC 2.7.4.6)	J05207	Myxococcus xanthus	451	62
ORF658	724246	723626	Holliday junction DNA helicase (ruvA)	U32716	Haemophilus influenzae	293	43
ORF659	724754	724251	crossover junction endodeoxyribonuclease (ruvC)	U32717	Haemophilus influenzae	296	53
ORF660	725868	724900	putative				
ORF661	727115	726270	putative				
ORF662	728126	727119	glyceraldehyde-3-phosphate dehydrogenase	U83198	Chlamydia trachomatis	1340	75
ORF663	728594	728208	ribosomal protein L17	L33834	Chlamydia trachomatis	439	82
ORF664	729614	728604	RNA polymerase alpha-subunit	L33834	Chlamydia trachomatis	1356	89
ORF665	729778	729533	RNA polymerase alpha-subunit	L33834	Chlamydia trachomatis	273	82
ORF666	730149	729751	ribosomal protein S11	L33834	Chlamydia trachomatis	562	90
ORF667	730539	730174	ribosomal protein S13	L33834	Chlamydia trachomatis	544	89
ORF668	731983	730598	homolog	L25077	Chlamydia trachomatis	1956	83
ORF669	732427	731996	ribosomal protein CtrL15e	M80325	Chlamydia trachomatis	563	77
ORF670	732917	732423	ribosomal protein CtrS5e	M80325	Chlamydia trachomatis	702	84
ORF671	733598	733320	ribosomal protein L6	M60652	Chlamydia trachomatis	316	87
ORF672	733869	733492	ribosomal protein L6	M60652	Chlamydia trachomatis	469	77
ORF673	734298	733900	ribosomal protein CtrS8e	M80325	Chlamydia trachomatis	572	82
ORF674	734858	734319	ribosomal protein CtrL5e	M80325	Chlamydia trachomatis	730	90
ORF675	735195	734863	ribosomal protein CtrL24e	M80325	Chlamydia trachomatis	420	70
ORF676	735578	735342	ribosomal protein CtrL14e	M80325	Chlamydia trachomatis	270	95
ORF677	735861	735604	ribosomal protein S17e	M80325	Chlamydia trachomatis	322	77
ORF678	736492	736079	50S ribosomal protein L16	D90905	Synechocystis sp.	439	60

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF679	737192	736524	ribosomal protein S3	D64071	Actinobacillus actinomycetemcomitans	612	58
ORF680	737555	737211	ribosomal protein L22	Z21677	Thermotoga maritima	228	48
ORF681	738688	737837	50S ribosomal subunit protein L2	U18997	Escherichia coli	769	62
ORF682	739048	738713	putative				
ORF683	739736	739065	ribosomal protein L4	X67014	Bacillus stearothermophilus	308	46
ORF684	740477	739773	ribosomal protein L3	Z46265	Thermus aquaticus thermophilus	463	50
ORF685	740659	740958	putative				
ORF686	741722	740721	putative				
ORF687	742789	741827	methionyl-tRNA formyltransferase	D64001	Synechocystis sp.	511	48
ORF688	743618	742782	UDP-N-acetylglucosamine acyltransferase	L22690	Rickettsia rickettsii	542	43
ORF689	744092	743634	(3R)-hydroxymyristol acyl carrier protein dehydrase	D90910	Synechocystis sp.	339	55
ORF690	744604	744107	UDP-3-0-acyl N-acetylglcosamine deacetylase	D90902	Synechocystis sp.	287	45
ORF691	744953	744498	UDP-3-O-acyl-GlcNAc deacetylase	U67855	Pseudomonas aeruginosa	262	51
ORF692	746608	744986	apolipoprotein N-acyltransferase (cute)	U32716	Haemophilus influenzae	194	50
ORF693	747085	746621	low homology to P14 protein of Heamophilus influenzar and 14.2 kDa protein of Escherichia coli	D78189	Bacillus subtilis	235	37
ORF694	747974	747219	polymerase III	M22996	Bacillus subtilis	180	34
ORF695	748594	748169	hypothetical protein	D90914	Synechocystis sp.	160	43
ORF696	749145	748573	putative				
ORF697	749652	749957	trxA	L39892	Chlamydia psittaci	393	72
ORF698	750446	749979	spoU	L39892	Chlamydia psittaci	559	72
ORF699	751219	750446	mip	L39892	Chlamydia psittaci	948	60
ORF700	753042	751291	aspartyl-tRNA synthetase	D90910	Synechocystis sp.	1347	47
ORF701	754309	753020	histidine--tRNA ligase	Z17214	Streptococcus equisimilis	757	44
ORF702	755120	756175	hexosephosphate transport protein	M89480	Salmonella typhimurium	870	49
ORF703	756120	756485	hexosephosphate transport protein	M89479	Escherichia coli	321	45
ORF704	756499	760227	DNA polymerase III alpha-subunit (dnaE)	AE000646	Helicobacter pylori	1977	42
ORF705	761217	760297	putative				
ORF706	761297	761809	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF707	761782	762282	putative				
ORF708	762260	762895	putative				
ORF709	762867	763316	hypothetical protein	D90908	Synechocystis sp.	177	43
ORF710	763780	763325	putative				
ORF711	763861	765168	DD-carboxypeptidase	M85047	Bacillus subtilis	292	37
ORF712	766809	765697	fmu and fmv protein	D90902	Synechocystis sp.	130	36
ORF713	768051	766888	putative				
ORF714	768566	768321	putative				
ORF715	769342	768551	putative				
ORF716	770532	769378	putative				
ORF717	771451	770804	putative				
ORF718	773058	771847	3-phosphoglycerate kinase	U83197	Chlamydia trachomatis	1540	72
ORF719	773094	773456	putative				
ORF720	774376	773093	putative phosphate permease	U84890	Mesembryanthemum crystallinum	870	45
ORF721	775123	774380	putative				
ORF722	775398	774916	putative				
ORF723	775046	776077	sporulation protein	M57689	Bacillus subtilis	698	43
ORF724	776070	777041	was dppE	U00039	Escherichia coli	565	56
ORF725	777964	777536	orf288; translated orf similarity to SWISS-PROT: YGI2_PSEPU hypothetical 32.4 kDa protein of Pseudomomas putida	Y10436	Coxiella burnetii	256	46
ORF726	778176	777904	B.subtilis genes rpmH, mpA, 50kd, gidA and gidB	X62539	Bacillus subtilis	112	37
ORF727	778621	779334	putative				
ORF728	781173	780307	f406; This 406 aa orf is 28 pct identical (12 gaps) to 264 residues of an approx. 440 aa protein YAOA_SCHPO SW: Q10089	AE000263	Escherichia coli	603	40
ORF729	781526	781116	f406; This 406 aa orf is 28 pct identical (12 gaps) to 264 residues of an approx. 440 aa protein YAOA_SCHPO SW: Q10089	AE000263	Escherichia coli	258	45
ORF730	782784	781555	f423; This 423 aa orf is 29 pct identical (1 gaps) to 172 residues of an approx. 488 aa protein YC24_CYAPA SW: P48260	AE000263	Escherichia coli	197	44

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF731	783572	782805	hypothetical chloroplast ORF 16	U38804	*Porphyra purpurea*	597	52
ORF732	785032	783581	ABC transporter subunit	D64004	*Synechocystis sp.*	1720	62
ORF733	786412	785360	putative				
ORF734	788429	786450	pbp	Y14206	*Streptomyces coelicolor*	148	55
ORF735	788944	788528	penicillin-binding protein 3	X84053	*Pseudomonas aeruginosa*	148	38
ORF736	789758	788901	putative				
ORF737	790332	791504	major outer membrane protein	M64064	*Chlamydia pneumoniae*	2028	99
ORF738	791846	792721	ribosomal protein S2	U60196	*Chlamydia trachomatis*	904	70
ORF739	792724	793569	elongation factor Ts	U60196	*Chlamydia trachomatis*	1023	71
ORF740	793580	794323	UMP kinase	U60196	*Chlamydia trachomatis*	891	72
ORF741	794304	794843	ribosome-releasing factor	U60196	*Chlamydia trachomatis*	673	73
ORF742	795217	795732	unknown	D26185	*Bacillus subtilis*	105	42
ORF743	795722	796795	unknown	D26185	*Bacillus subtilis*	208	33
ORF744	798735	797053	putative	L33796	*Vibrio cholerae*	386	34
ORF745	799823	798681	putative				
ORF746	799297	799578	putative				
ORF747	801313	799808	Pkn5	U40656	*Myxococcus xanthus*	345	33
ORF748	802453	801332	putative				
ORF749	803299	802457	putative				
ORF750	803811	803290	putative				
ORF751	805151	803826	YscN	U02499	*Yersinia enterocolitica*	1185	53
ORF752	805860	805156	putative				
ORF753	806604	806332	putative				
ORF754	806913	806608	putative				
ORF755	808222	806903	putative				
ORF756	808751	808146	putative				
ORF757	809437	808673	putative				
ORF758	809939	809454	putative				
ORF759	811235	810213	delta-aminolevulinate synthase (EC 2.3.1.37)	M30785	*Escherichia coli*	172	40
ORF760	811779	813056	DNA gyrase subunit B	U35453	*Clostridium acetobutylicum*	584	38
ORF761	812890	812516	putative				
ORF762	812954	813583	DNA gyrase subunit B	Z19108	*Spiroplasma citri*	371	39

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF763	813587	815023	gyrA	X92503	Mycobacterium smegmatis	414	55
ORF764	815420	815746	putative				
ORF765	816036	817010	orf-X; hypothetical protein; Method: conceptual translation supplied by author	U48870	Bacillus subtilis	569	47
ORF766	817111	817356	unknown	Z74024	Mycobacterium tuberculosis	114	34
ORF767	817791	818609	3-deoxy-d-manno-octulosonic acid 8-phosphate synthetase	Z50747	Chlamydia psittaci	1112	78
ORF768	818609	819094	protein of unknown function	Z50747	Chlamydia psittaci	545	65
ORF769	819104	819823	ATP binding protein	U72493	Chlamydia trachomatis	1099	88
ORF770	820722	819826	putative				
ORF771	822313	821000	putative				
ORF772	823503	822238	putative				
ORF773	823678	825612	putative				
ORF774	825461	826312	putative				
ORF775	827280	826645	putative				
ORF776	828604	827171	76 kDa protein	L23921	Chlamydia pneumoniae	2179	100
ORF777	830026	828713	76 kDa protein	L23921	Chlamydia pneumoniae	1162	100
ORF778	831047	830085	mviB homolog	U50732	Chlamydia trachomatis	982	58
ORF779	831725	831051	mviB homolog	U50732	Chlamydia trachomatis	740	65
ORF780	832220	833098	T05H10.2	Z47812	Caenorhabditis elegans	407	34
ORF781	833851	833396	ribosomal protein S4 (rps4)	AE000633	Helicobacter pylori	372	53
ORF782	834068	835039	This ORF is homologous to a 40.0 kd hypothetical protein in the htrB 3' region from E. coli. Accession Number X61000	L22217	Mycoplasma-like organism	377	49
ORF783	835792	835127	uridine kinase	L31783	Mus musculus	436	43
ORF784	837624	836116	ORF f397	U29581	Escherichia coli	92	38
ORF785	838951	840882	putative				
ORF786	840869	842185	exodeoxyribonuclease V (recB)	U32811	Haemophilus influenzae	409	40
ORF787	841989	843455	DNA helicase II	U39703	Mycoplasma genitalium	110	46
ORF788	843242	844021	exodeoxyribonuclease V (recB)	U32811	Haemophilus influenzae	196	40
ORF789	845018	843987	MreC protein	M31792	Escherichia coli	76	53
ORF790	846174	844990	aspartate aminotransferase (aspC)	X03629	Escherichia coli	754	40
ORF791	848509	846311	GreA	U02878	Rickettsia prowazekii	190	35

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF792	848568	849014	putative				
ORF793	849082	850488	NADH:ubiquinone oxidoreducatase subunit A (GP:Z37111 2)	U32702	Haemophilus influenzae	445	37
ORF794	851512	850574	porphobilinogen synthase	U38348	Chlorobium vibrioforme	769	45
ORF795	852064	852447	putative				
ORF796	852398	853690	putative				
ORF797	855118	854243	geranylgeranyl pyrophosphate synthase	D85029	Arabidopsis thaliana	408	41
ORF798	855751	855128	f147; This 147 aa orf is 26 pct identical (1 gaps) to 99 residues of an approx. 728 aa protein E2BE RABIT SW: P47823	AE000143	Escherichia coli	187	36
ORF799	856551	855829	membrane associated regulatory protein	M28368	Salmonella typhimurium	172	36
ORF800	856730	858556	unknown function	Z32530	Chlamydia trachomatis	842	35
ORF801	858717	859601	exodeoxyribonuclease V (recD)	U32811	Haemophilus influenzae	182	51
ORF802	859591	860205	exonuclease V alpha subunit (AA 1-608)	X04582	Escherichia coli	235	45
ORF803	861132	860284	putative				
ORF804	861426	861163	30S ribosomal protein S20	Z67753	Odontella sinensis	153	41
ORF805	861701	862921	putative				
ORF806	863026	864798	major sigma factor	U04442	Chlamydia psittaci	2661	94
ORF807	864831	865256	putative				
ORF808	865226	866581	dihydropterin pyrophosphokinase /dihydropteroate synthase	Y08611	Pisum sativum	455	48
ORF809	866562	867119	dehydrofolate reductase, type I (folA)	U32772	Haemophilus influenzae	213	49
ORF810	867025	867816	M. jannaschii predicted coding region MJ0768	U67522	Methanococcus jannaschii	207	36
ORF811	867820	868497	putative				
ORF812	869743	868661	RecA	U16739	Chlamydia trachomatis	1512	87
ORF813	870633	870094	unknown function	Z32530	Chlamydia trachomatis	308	45
ORF814	871929	870646	unknown function	Z32530	Chlamydia trachomatis	1410	63
ORF815	872538	872086	putative				
ORF816	873908	872517	putative				
ORF817	874281	874670	nifR3-like gene product	Z37984	Azospirillum brasilense	181	32
ORF818	874582	875286	ORF1 gene product	X62399	Escherichia coli	307	42
ORF819	877857	875377	DNA topoisomerase 1	L27797	Bacillus subtilis	1488	50

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF820	878446	879255	putative				
ORF821	880635	879268	sigma factor (ntrA) (AA 1-502)	X05888	Azotobacter vinelandii	257	47
ORF822	882524	880593	DNA helicase II	D90906	Synechocystis sp.	1140	50
ORF823	882612	883319	ipa-57d gene product	X73124	Bacillus subtilis	601	51
ORF824	884155	883538	hypothetical protein	D90915	Synechocystis sp.	344	39
ORF825	884340	885611	19/20 residue stretch (32-51) identical to N-terminal putative signal sequence of unknown, partly cloned B. subtilis gene.; nutative	L19954	Bacillus subtilis	456	37
ORF826	885722	887302	heat shock protein	L12004	Chlamydia trachomatis	915	39
ORF827	887587	888153	bas1 protein	Z34917	Hordeum vulgare	474	50
ORF828	888627	888220	putative				
ORF829	889330	888716	hypothetical protein	Y14079	Bacillus subtilis	223	55
ORF830	889898	889323	peptidoglycan-associated lipoprotein	X65796	Escherichia coli	222	50
ORF831	891190	889898	TolB	U32470	Haemophilus influenzae	280	35
ORF832	891828	891247	putative				
ORF833	892421	892017	exbD peptide	M28819	Escherichia coli	77	48
ORF834	893116	892421	inner membrane protein (tolQ)	U32722	Haemophilus influenzae	157	54
ORF835	892521	892925	putative				
ORF836	893392	895419	inner membrane copper tolerance protein	Z36905	Escherichia coli	120	35
ORF837	895745	896527	unknown	D26185	Bacillus subtilis	381	41
ORF838	896668	897558	succinate dehydrogenase subunit C	Y08563	Paenibacillus macerans	253	40
ORF839	897565	899442	succinate dehydrogenase subunit A	Y08563	Paenibacillus macerans	1667	57
ORF840	899420	900229	succinate dehydrogenase subunit B	Y08563	Paenibacillus macerans	656	54
ORF841	903230	900237	putative				
ORF842	905081	903234	putative				
ORF843	906931	905045	sigma factor SibG regulation protein RsbU	D90905	Synechocystis sp.	117	35
ORF844	907248	907832	putative				
ORF845	907784	908128	putative				
ORF846	908132	908677	putative				
ORF847	908589	909320	putative				
ORF848	909405	911465	putative				
ORF849	911677	912360	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF850	912303	912821	putative				
ORF851	912937	913983	putative				
ORF852	915128	914067	putative				
ORF853	916658	915303	enolase	L29475	Bacillus subtilis	1036	60
ORF854	915627	915376	enolase	U43738	Mycoplasma pneumoniae	226	65
ORF855	917707	916853	excinuclease ABC subunit B (uvrB)	U32804	Haemophilus influenzae	724	46
ORF856	918837	917722	excinuclease ABC subunit B (uvrB)	U32804	Haemophilus influenzae	1029	54
ORF857	919868	918837	tryptophanyl-tRNA synthetase (trpS)	U32746	Haemophilus influenzae	376	40
ORF858	920434	919880	putative				
ORF859	921187	920438	ORF8	X82078	Chlamydia sp.	164	50
ORF860	921959	921195	hypothetical protein	X62475	Chlamydia psittaci	511	44
ORF861	923773	921995	Threonyl tRNA Synthetase	Z80360	Bacillus subtilis	1476	44
ORF862	922146	922415	putative				
ORF863	923943	923674	putative				
ORF864	924077	925006	putative				
ORF865	925436	925083	putative				
ORF866	926524	925349	putative				
ORF867	927920	926433	putative				
ORF868	928319	927951	putative				
ORF869	928963	928334	putative				
ORF870	929248	930987	DNA mismatch repair protein (mutL)	U32692	Haemophilus influenzae	585	40
ORF871	930995	932059	YqhT	D84432	Bacillus subtilis	445	39
ORF872	932121	933515	putative				
ORF873	932881	932513	putative				
ORF874	933485	935746	pulD (ttg start codon)	M32613	Klebsiella pneumoniae	210	33
ORF875	935724	937082	epsE	M96172	Vibrio cholerae	890	55
ORF876	937229	938410	PilG	U32588	Neisseria gonorrhoeae	280	38
ORF877	938281	938805	putative				
ORF878	938809	939255	putative				
ORF879	939165	939782	putative				
ORF880	939760	940791	putative				
ORF881	940822	941106	putative				
ORF882	940977	941351	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF883	942537	941623	yscT	L25667	Yersinia pseudotuberculosis	169	44
ORF884	942784	942500	yscS	L25667	Yersinia pseudotuberculosis	173	42
ORF885	943149	942799	HrcR	AE000107	Rhizobium sp. NGR234	265	52
ORF886	943799	943029	pathogenicity protein	M64094	Xanthomonas campestris	252	41
ORF887	944055	943732	putative	M74011	Yersinia enterocolitica	112	33
ORF888	944413	943994	putative				
ORF889	945395	944556	putative				
ORF890	945853	945389	putative				
ORF891	946392	945751	HrcJ	U56662	Erwinia amylovora	229	44
ORF892	947410	948081	putative				
ORF893	949871	948915	ORF YOR196c	Z75104	Saccharomyces cerevisiae	702	44
ORF894	951058	949868	dihydrolipoamide dehydrogenase E3 subunit	M57435	Bacillus subtilis	745	39
ORF895	951249	950959	dihydrolipoamide acetyltransferase E3 subunit	M73535	Staphylococcus aureus	166	49
ORF896	951664	952134	putative				
ORF897	952674	952165	SNF	X98455	Bacillus cereus	229	47
ORF898	953491	952589	helicase	U39680	Mycoplasma genitalium	307	42
ORF899	955324	953495	F01G4.1	Z68341	Caenorhabditis elegans	133	57
ORF900	955823	955281	putative				
ORF901	957082	955847	branched-chain amino acid carrier	Z48676	Lactobacillus delbrueckii	297	40
ORF902	957902	957270	endonuclease III	U11289	Bacillus subtilis	317	37
ORF903	959231	957906	homologous to E.coli 50K	X62539	Bacillus subtilis	805	45
ORF904	959376	960284	phosphatidylserine decarboxylase	U72715	Chlamydia trachomatis	776	51
ORF905	960266	961669	putative				
ORF906	961856	964765	secretory component	U06928	Caulobacter crescentus	1812	55
ORF907	966855	965395	28.2% of identity to the Escherichia coli GTP-binding protein Era: putative	L47648	Bacillus subtilis	778	41
ORF908	968204	966975	poly(A) polymerase	L47709	Bacillus subtilis	383	41
ORF909	968791	968237	ClpX-like protein	U18229	Bacillus subtilis	340	39
ORF910	969498	968731	ATP-dependent protease ATPase subunit	D64006	Synechocystis sp.	846	66
ORF911	969858	969511	ClpP	U16135	Synechococcus sp.	257	54

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF912	970118	969762	ATP-dependent clp protease proteolytic component (clpP)	AE000591	Helicobacter pylori	362	63
ORF913	970593	970300	putative				
ORF914	971261	970542	putative				
ORF915	971680	971123	putative				
ORF916	971876	975100	SNF	X98455	Bacillus cereus	778	49
ORF917	975419	976516	MreB protein	M96343	Bacillus subtilis	960	55
ORF918	976584	978320	phospho enol pyruvate carboxykinase	S56812	Chlorobium limicola	1667	64
ORF919	977680	977231	putative				
ORF920	978399	980738	putative				
ORF921	980756	981928	putative				
ORF922	982974	981931	precursor protein (AA -22 to 371)	X52557	Chlamydia trachomatis	97	50
ORF923	984120	983119	NAD+ dependent glycerol-3-phosphate dehydrogenase	L47648	Bacillus subtilis	618	43
ORF924	985502	984120	AgX-1 antigen [human, infertile patient, testis. Peptide. 505 aa]	S73498	Homo sapiens	254	34
ORF925	987180	985882	ORF 4	M72718	Bacillus subtilis	697	38
ORF926	987172	987444	putative				
ORF927	989846	989049	nifU-like protein	AE000542	Helicobacter pylori	302	31
ORF928	991048	989846	putative				
ORF929	991638	990955	phosphoglyceromutase	L09651	Zymomonas mobilis	471	53
ORF930	991794	992498	ORFX13	L09228	Bacillus subtilis	403	39
ORF931	993619	993041	biotin [acetyl-CoA-carboxylase] ligase	L47709	Bacillus subtilis	136	38
ORF932	993530	994792	rod-shape-determining protein	M22857	Escherichia coli	312	44
ORF933	995970	994795	cadmium-transporting ATPase	D64005	Synechocystis sp.	358	47
ORF934	996857	995739	ATPase	L28104	Transposon Tn5422	449	39
ORF935	997603	996782	putative				
ORF936	998969	997572	seryl-trna synthetase	Y09924	Staphylococcus aureus	851	42
ORF937	998896	1000023	orf2, homologue to B.subtilis ribG	X64395	Escherichia coli	596	40
ORF938	1000087	1001340	GTP cyclohydrolase II	D90912	Synechocystis sp.	1078	52
ORF939	1001357	1001818	riboflavin synthase beta subunit	U27202	Actinobacillus pleuropneumoniae	278	36
ORF940	1003288	1001873	putative				
ORF941	1003487	1004146	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF942	1004485	1005639	D-alanine glycine permease (dagA)	AE000603	Helicobacter pylori	394	33
ORF943	1005643	1005972	hypothetical protein MTCY180.08	Z97193	Mycobacterium tuberculosis	274	58
ORF944	1006784	1006116	similar to trithorax protein in final three exons	U13875	Caenorhabditis elegans	155	46
ORF945	1007563	1006769	yycJ	D78193	Bacillus subtilis	406	38
ORF946	1009226	1007568	YtpI	AF008220	Bacillus subtilis	992	47
ORF947	1009989	1009336	putative				
ORF948	1015852	1016337	putative				
ORF949	1016561	1016181	putative				
ORF950	1016297	1017532	putative				
ORF951	1016802	1016452	putative				
ORF952	1018993	1017701	phenolhydroxylase component	U32702	Haemophilus influenzae	909	47
ORF953	1019454	1019137	ORF	M63939	Escherichia coli	96	45
ORF954	1020764	1019562	pCTHom1 gene product	M94254	Chlamydia trachomatis	1185	65
ORF955	1021405	1021037	histone H1-like protein	M80324	Chlamydia psittaci	319	62
ORF956	1021821	1024286	phosphoprotein	L25078	Chlamydia trachomatis	739	41
ORF957	1024697	1024248	putative				
ORF958	1025569	1024508	protoporphyrinogen oxidase	U25114	Mus musculus	86	38
ORF959	1026969	1025590	oxygen independent coprophorphyrinogen III oxidase	D90912	Synechocystis sp.	880	42
ORF960	1027789	1026947	uroporphyrinogen decarboxylase	M97208	Bacillus subtilis	372	38
ORF961	1031199	1027945	transcription-repair coupling factor (trcF) (mfd)	U32805	Haemophilus influenzae	1584	42
ORF962	1031717	1031172	alanyl-tRNA synthetase	X95571	Thiobacillus ferrooxidans	76	31
ORF963	1033057	1031612	alanyl-tRNA synthetase	AE000353	Escherichia coli	889	40
ORF964	1033425	1033039	alanyl-tRNA synthetase (alaS)	AE000629	Helicobacter pylori	327	51
ORF965	1033784	1033200	alanyl-tRNA synthetase	X59956	Rhizobium leguminosarum	416	47
ORF966	1033963	1036038	transketolase	Z73234	Bacillus subtilis	1398	44
ORF967	1036945	1036010	AMP nucleosidase	AE000290	Escherichia coli	265	42
ORF968	1037110	1037679	elongation factor P	U14003	Escherichia coli	458	51
ORF969	1037696	1037944	putative				
ORF970	1038916	1037975	putative				
ORF971	1040582	1039026	HSP60 chaperonin	X62914	Clostridium perfringens	284	31

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF972	1040997	1042337	PROBABLE UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMYL-2, 6-DIAMINOLIGASE (EC 6.3.2.15).	AB001488	Bacillus subtilis	446	39
ORF973	1042357	1043403	ORF-Y (AA 1-360)	X51584	Escherichia coli	582	45
ORF974	1043367	1044623	UDP-N-acetylmuramoylalanine-D-glutamate ligase (murD)	U32793	Haemophilus influenzae	348	42
ORF975	1044607	1045362	hypothetical protein	Y14079	Bacillus subtilis	115	38
ORF976	1045384	1046538	spoVE gene product (AA 1-366)	X51419	Bacillus subtilis	479	35
ORF977	1046447	1047517	mur	Y13922	Enterococcus hirae	256	45
ORF978	1047521	1049956	UDP-N-acetylmuramate-alanine ligase (murC)	U32794	Haemophilus influenzae	756	38
ORF979	1050611	1050036	unknown	Z74024	Mycobacterium tuberculosis	78	44
ORF980	1050925	1050566	cycY gene product	U14003	Escherichia coli	179	34
ORF981	1051728	1051090	putative				
ORF982	1051743	1052063	hypothetical protein	D90908	Synechocystis sp.	135	33
ORF983	1052101	1053126	trna delta(2)-isopentenylpyrophosphate transferase	Z98209	Mycobacterium tuberculosis	441	37
ORF984	1054201	1053107	conserved hypothetical protein	AE000579	Helicobacter pylori	826	44
ORF985	1054242	1055555	putative				
ORF986	1055483	1055908	putative				
ORF987	1056609	1056965	YqeL	D84432	Bacillus subtilis	202	38
ORF988	1056961	1058232	beta-ketoacyl-ACP synthase	L13242	Ricinus communis	1266	55
ORF989	1058238	1058687	diadenosine tetraphosphatase	U30313	Homo sapiens	122	42
ORF990	1059371	1058727	inorganic pyrophosphatase (ppa)	AE000576	Helicobacter pylori	209	39
ORF991	1059526	1060578	leucine dehydrogenase LeuDH	U51099	Bacillus cereus	680	45
ORF992	1061553	1060579	3'(2'),5'-bisphosphate nucleotidase	U40433	Arabidopsis thaliana	335	43
ORF993	1061674	1062411	putative				
ORF994	1062377	1064077	2-acylglycerophosphoethanolamine acyl transferase/acyl carrier protein synthetase	U29581	Escherichia coli	383	44
ORF995	1064116	1065243	7-keto-8-aminopelargonic acid synthetase (bioF)	M29291	Bacillus sphaericus	200	35
ORF996	1067451	1065178	priA	Y10304	Bacillus subtilis	1009	43

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF997	1068065	1067376	putative				
ORF998	1068209	1068706	putative				
ORF999	1069958	1068819	unknown	U41759	Chlamydia psittaci	777	41
ORF1000	1071163	1070033	unknown	U41759	Chlamydia psittaci	381	36
ORF1001	1072438	1071332	unknown	U41759	Chlamydia psittaci	254	37
ORF1002	1072997	1073476	putative				
ORF1003	1074239	1075864	lysyl-tRNA synthetase	D90906	Synechocystis sp.	1007	48
ORF1004	1076790	1075867	cysteinyl-tRNA synthetase	L14580	Bacillus subtilis	395	52
ORF1005	1077268	1076573	cys-tRNA synthetase (cysS)	U32693	Haemophilus influenzae	431	56
ORF1006	1077999	1078724	putative				
ORF1007	1079088	1078672	ribonuclease P protein component (gtg start codon)	M11056	Escherichia coli	78	46
ORF1008	1079642	1079944	30S ribosomal subunit protein S14	U18997	Escherichia coli	260	50
ORF1009	1080501	1079995	F18C12.2	Z75536	Caenorhabditis elegans	118	38
ORF1010	1080775	1081341	putative				
ORF1011	1083158	1081350	deoxyribodipyrimidine photolyase	J03294	Bacillus subtilis	687	44
ORF1012	1084677	1083235	DNA mismatch repair protein	U71154	Aquifex pyrophilus	735	48
ORF1013	1085648	1084632	DNA mismatch repair protein	D90909	Synechocystis sp.	565	39
ORF1014	1086117	1086737	DNA primase (dnaG)	U32735	Haemophilus influenzae	303	40
ORF1015	1086692	1087897	DnaG	Z83860	Mycobacterium tuberculosis	222	37
ORF1016	1088646	1089005	putative				
ORF1017	1089146	1089805	putative				
ORF1018	1092931	1089890	glycyl-tRNA synthetase	U20547	Chlamydia trachomatis	2569	48
ORF1019	1093179	1092889	putative				
ORF1020	1093584	1094204	phosphatidylglycerophosphate synthase	U87792	Bacillus subtilis	163	55
ORF1021	1095619	1094192	glycogen (starch) synthase	D90899	Synechocystis sp.	574	40
ORF1022	1096074	1096628	partial ctc gene product (AA 1-186)	X16518	Bacillus subtilis	86	37
ORF1023	1096633	1097082	peptidyl-tRNA hydrolase	U31570	Chlamydia trachomatis	378	53
ORF1024	1097266	1097601	ribosomal protein S6 (rps6)	AE000630	Helicobacter pylori	179	39
ORF1025	1097622	1097867	ribosomal protein S18 homolog; putative	M62820	Chlamydia trachomatis	324	86
ORF1026	1097886	1098392	putative heat shock protein ORF; putative	M62820	Chlamydia trachomatis	190	79
ORF1027	1099521	1099279	putative				
ORF1028	1099689	1101053	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1029	1102192	1101107	putative				
ORF1030	1104950	1102116	glycerol-3-phosphate acyltransferase	M80571	Cucumis sativus	574	43
ORF1031	1106508	1104946	ORF_f495; orfF of ECMRED, uses 2nd start	U18997	Escherichia coli	855	38
ORF1032	1106722	1107249	putative				
ORF1033	1107463	1108101	PlsX	U59433	Bacillus subtilis	282	45
ORF1034	1108041	1108421	fatty acid/phospholipid synthesis protein (plsX)	AE000540	Helicobacter pylori	205	35
ORF1035	1108520	1113370	putative 98 kDa outer membrane protein	U72499	Chlamydia psittaci	352	44
ORF1036	1114958	1113447	putative				
ORF1037	1116915	1115071	lipid A disaccharide synthetase (lpxB)	U32786	Haemophilus influenzae	477	42
ORF1038	1118183	1116894	poly(A) polymerase	AE000123	Escherichia coli	555	46
ORF1039	1118846	1120030	putative	L12968	Escherichia coli	880	50
ORF1040	1120040	1120522	glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS)	AE000651	Helicobacter pylori	396	52
ORF1041	1120510	1121430	glutamine amidotransferase; glucosamine--fructose-6-phosphate aminotransferase	AE000450	Escherichia coli	494	44
ORF1042	1121321	1121866	L-glutamine:D-fructose-6-P amidotransferase precursor	U17352	Thermus aquaticus thermophilus	374	50
ORF1043	1122123	1122899	tyrosine-specific transport protein	AE000284	Escherichia coli	281	41
ORF1044	1124842	1125564	putative				
ORF1045	1126526	1125579	cell division protein (ftsY)	U32760	Haemophilus influenzae	497	41
ORF1046	1126519	1127676	succinyl-CoA synthetase beta-subunit	J01619	Escherichia coli	784	43
ORF1047	1127672	1128571	succinyl coenzyme A synthetase alpha subunit	U23408	Dictyostelium discoideum	978	63
ORF1048	1130230	1131336	putative				
ORF1049	1131480	1132553	putative				
ORF1050	1132830	1133843	putative				
ORF1051	1134121	1134855	serine protease HtrA	D90905	Synechocystis sp.	307	51
ORF1052	1134642	1135592	GsrA protein	D78376	Yersinia enterocolitica	497	41
ORF1053	1135964	1135653	putative				
ORF1054	1137132	1135954	R11H6.1	Z93386	Caenorhabditis elegans	445	37
ORF1055	1137169	1140102	Ydr430cp; CAI: 0.15	U33007	Saccharomyces cerevisiae	559	40

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1056	1141365	1140112	hypothetical 54.7 kD protein in udp 3' region precursor (o475)	AE000459	Escherichia coli	222	34
ORF1057	1142150	1141356	phosphatidylserine synthase (pssA)	AE000614	Helicobacter pylori	307	41
ORF1058	1142520	1145660	ribonucleotide reductase subunit M1	K02927	Mus musculus	1433	45
ORF1059	1145627	1146721	ribonucleoside diphosphate reductase, beta subunit (nrdB)	AE000553	Helicobacter pylori	443	32
ORF1060	1146862	1147545	unknown	Z95398	Mycobacterium leprae	191	35
ORF1061	1147666	1148190	YtqB	AF008220	Bacillus subtilis	262	44
ORF1062	1148514	1148224	ORF2	U01958	Bacillus licheniformis	135	54
ORF1063	1149136	1148348	ORF2	M31827	Bacillus subtilis	268	40
ORF1064	1149702	1149166	putative				
ORF1065	1150031	1150591	unknown	Z85982	Mycobacterium tuberculosis	445	49
ORF1066	1150785	1151147	ribosomal protein L20 (AA 1-119)	X16188	Bacillus stearothermophilus	273	44
ORF1067	1151165	1152181	phenylalany-tRNA synthetase beta subunit	Z75208	Bacillus subtilis	777	40
ORF1068	1152522	1154591	putative				
ORF1069	1155666	1154566	putative				
ORF1070	1156743	1155670	putative				
ORF1071	1156859	1157815	hypothetical	U32723	Haemophilus influenzae	252	42
ORF1072	1157982	1160735	ATP-binding protein	U01376	Escherichia coli	1314	56
ORF1073	1162620	1160917	polynucleotide phosphorylase	AF010578	Pisum sativum	1416	52
ORF1074	1162970	1162590	polyribonucleotide phophorylase	U52048	Spinacia oleracea	312	53
ORF1075	1163532	1164020	orf150 gene product	X95938	Porphyromonas gingivalis	335	43
ORF1076	1163995	1164294	putative				
ORF1077	1165569	1165030	putative				
ORF1078	1166108	1165566	putative				
ORF1079	1166644	1166141	putative				
ORF1080	1167055	1168374	putative				
ORF1081	1169218	1168337	methionine aminopeptidase	D64003	Synechocystis sp.	488	54
ORF1082	1169823	1169218	ORF o197	U18997	Escherichia coli	281	30
ORF1083	1171324	1170572	putative				
ORF1084	1172085	1171177	hypothetical	U32720	Haemophilus influenzae	162	44
ORF1085	1172394	1173773	fumarase	D64000	Synechocystis sp.	1292	57
ORF1086	1175209	1173881	prs-associated putative membrane protein	U02424	Escherichia coli	570	39

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1087	1175555	1175127	hypothetical protein in pth-prs intergenic region	AE000219	Escherichia coli	278	46
ORF1088	1175778	1177043	hypothetical protein	Z96072	Mycobacterium tuberculosis	109	43
ORF1089	1177177	1179048	putative				
ORF1090	1179156	1180085	penicillin tolerance protein (lytB)	U32781	Haemophilus influenzae	731	54
ORF1091	1180045	1180779	putative				
ORF1092	1181942	1180788	putative				
ORF1093	1182296	1181961	putative				
ORF1094	1183844	1182300	putative				
ORF1095	1184420	1183848	putative				
ORF1096	1185382	1184366	putative				
ORF1097	1185858	1185226	putative				
ORF1098	1186164	1186481	putative				
ORF1099	1187386	1186484	site-specific recombinase	U92524	Salmonella typhimurium	401	48
ORF1100	1187370	1189028	phophoglucoisomerase-like protein	L40822	Chlamydia trachomatis	1154	63
ORF1101	1189321	1190889	putative				
ORF1102	1191142	1192146	NADP-malate dehydrogenase	L40958	Flaveria bidentis	775	46
ORF1103	1191974	1191729	putative				
ORF1104	1193815	1192991	putative				
ORF1105	1195702	1194248	o460; This 460 aa orf is 46 pct identical (26 gaps) to 458 residues of an approx. 488 aa protein ARCD PSEAE SW: P18275	AE000256	Escherichia coli	1022	44
ORF1106	1196303	1195716	putative				
ORF1107	1196831	1196337	putative				
ORF1108	1197807	1196746	putative				
ORF1109	1198740	1197883	putative				
ORF1110	1200232	1198721	shikimate 5-dehydrogenase	U67551	Methanococcus jannaschii	245	37
ORF1111	1201286	1200135	3-dehydroquinate synthase (aroB)	U32705	Haemophilus influenzae	478	45
ORF1112	1202386	1201259	2,3-dihydroxybenzoic acid	L29562	Vibrio anguillarum	780	50
ORF1113	1202901	1202350	putative				
ORF1114	1204162	1202816	5-enolpyruvylshikimate 3-phosphate synthase	U67500	Methanococcus jannaschii	520	40
ORF1115	1203177	1203464	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1116	1205028	1204180	putative				
ORF1117	1206392	1204878	bioA gene product	A02587	unidentified	834	48
ORF1118	1206742	1206086	dethiobiotin synthase (bioD)	U32830	Haemophilus influenzae	243	37
ORF1119	1207872	1206724	L-alanine - pimelyl CoA ligase	U51868	Bacillus subtilis	601	41
ORF1120	1208852	1207851	biotin sythase	U24147	Arabidopsis thaliana	892	52
ORF1121	1210518	1209742	tryptophan hydroxylase	U26428	Gallus gallus	237	34
ORF1122	1210703	1211494	dihydrodipicolinate reductase	U47017	Pseudomonas syringae pv. tabaci	345	37
ORF1123	1211870	1212754	aspartate-semialdehyde dehydrogenase	U67476	Methanococcus jannaschii	444	43
ORF1124	1212742	1214064	aspartokinase III	U00006	Escherichia coli	473	47
ORF1125	1214046	1214858	dihydrodipicolinate synthase	D64006	Synechocystis sp.	238	40
ORF1126	1215551	1216318	putative				
ORF1127	1216493	1216849	putative				
ORF1128	1217183	1219612	putative				
ORF1129	1220068	1219673	putative				
ORF1130	1219710	1220669	putative				
ORF1131	1220630	1221376	putative				
ORF1132	1221645	1223681	unknown	D26185	Bacillus subtilis	621	43
ORF1133	1223894	1224988	putative				
ORF1134	1225000	1225830	high level kasgamycin resistance	D26185	Bacillus subtilis	422	41
ORF1135	1227810	1225879	hypothetical protein	D90903	Synechocystis sp.	1129	43
ORF1136	1226528	1226908	putative				
ORF1137	1229972	1228311	exonuclease VII, large subunit (xseA)	U32723	Haemophilus influenzae	666	46
ORF1138	47569	47018	Integrase/recombinase	AE001308	Chlamydia trachomatis	716	72
ORF1139	49980	49117	putative				
ORF1140	53356	52898	putative				
ORF1141	54477	54884	O-Sialoglycoprotein Endopeptidase	AE001307	Chlamydia trachomatis	311	51
ORF1142	63753	63998	PTS PEP Phosphotransferase	AE001306	Chlamydia trachomatis	198	61
ORF1143	77164	77487	putative				
ORF1144	79724	79302	Sms Protein	AE001302	Chlamydia trachomatis	458	57
ORF1145	88721	88951	putative				
ORF1146	94067	94429	putative				
ORF1147	122832	123341	hypothetical protein	AE001303	Chlamydia trachomatis	398	61
ORF1148	147536	147234	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1149	158990	159346	S16 Ribosomal Protein	AE001277	*Chlamydia trachomatis*	467	78
ORF1150	168470	168979	putative				
ORF1151	169183	169452	putative				
ORF1152	171785	171504	Cationic Amino Acid Transporter	AE001278	*Chlamydia trachomatis*	262	68
ORF1153	172518	171775	Cationic Amino Acid Transporter	AE001278	*Chlamydia trachomatis*	533	48
ORF1154	193599	194045	putative				
ORF1155	195704	196075	S/T Protein Kinase	AE001288	*Chlamydia trachomatis*	536	82
ORF1156	210687	210145	KDO-transferase	X80061	*Chlamydia pneumoniae*	856	96
ORF1157	211100	210708	putative				
ORF1158	215420	215088	putative				
ORF1159	217914	218246	putative				
ORF1160	218925	218701	putative				
ORF1161	223785	223525	IMP dehydrogenase	U13372	*Borrelia burgdorferi*	270	63
ORF1162	224271	223999	putative				
ORF1163	228691	228407	putative				
ORF1164	235050	235334	(Methylase)	AE001287	*Chlamydia trachomatis*	331	66
ORF1165	252308	253021	Oligopeptide Permease	AE001293	*Chlamydia trachomatis*	838	72
ORF1166	258280	258912	Dicarboxylate Translocator	AE001294	*Chlamydia trachomatis*	909	80
ORF1167	261325	261567	putative				
ORF1168	268195	268878	hypothetical protein	AE001287	*Chlamydia trachomatis*	556	52
ORF1169	269447	268881	putative				
ORF1170	271263	271538	putative				
ORF1171	271957	272346	putative				
ORF1172	274176	274550	putative				
ORF1173	275736	275314	Disulfide bond Oxidoreductase	AE001291	*Chlamydia trachomatis*	519	73
ORF1174	276490	276927	hypothetical protein	AE001291	*Chlamydia trachomatis*	249	53
ORF1175	277577	277861	hypothetical protein	AE001291	*Chlamydia trachomatis*	256	52
ORF1176	288163	287909	putative				
ORF1177	290130	289789	putative				
ORF1178	290989	291225	putative				
ORF1179	291372	291860	adenylate cyclase	AE001286	*Chlamydia trachomatis*	388	48
ORF1180	311239	311622	putative				
ORF1181	328665	328384	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1182	337348	338289	sodium-dependent transporter	AF017105	Chlamydia psittaci	1112	72
ORF1183	364764	364369	Prolipoprotein Diacylglycerol Transferase	AE001298	Chlamydia trachomatis	300	54
ORF1184	389623	390135	hypothetical protein	AE001282	Chlamydia trachomatis	75	33
ORF1185	393729	394343	ABC superfamily ATPase	AE001282	Chlamydia trachomatis	473	52
ORF1186	407379	407621	putative				
ORF1187	410944	410708	putative				
ORF1188	427632	427988	putative				
ORF1189	428172	428486	putative				
ORF1190	436761	437246	hypothetical protein	AE001279	Chlamydia trachomatis	661	81
ORF1191	460911	461159	putative				
ORF1192	477597	477313	hypothetical protein	AE001300	Chlamydia trachomatis	309	62
ORF1193	487303	487001	putative				
ORF1194	487764	487534	Glycine Cleavage System H Protein	AE001300	Chlamydia trachomatis	221	67
ORF1195	498502	499017	hypothetical protein	AE001275	Chlamydia trachomatis	206	32
ORF1196	499795	500466	putative				
ORF1197	571928	572344	putative				
ORF1198	572367	572131	putative				
ORF1199	588184	587915	hypothetical protein	AE001312	Chlamydia trachomatis	256	62
ORF1200	600587	600907	(Metalloenzyme)	AE001316	Chlamydia trachomatis	314	61
ORF1201	609731	608895	putative				
ORF1202	614039	614755	hypothetical protein	AE001317	Chlamydia trachomatis	475	46
ORF1203	614823	615152	putative				
ORF1204	638244	638831	ABC Transporter ATPase	AE001315	Chlamydia trachomatis	614	61
ORF1205	638819	639094	(Metal Transport Protein)	AE001315	Chlamydia trachomatis	265	63
ORF1206	639073	639636	(Metal Transport Protein)	AE001315	Chlamydia trachomatis	687	69
ORF1207	647901	648236	hypothetical protein	AE001317	Chlamydia trachomatis	139	38
ORF1208	678510	679469	phosphohydrolase	AE001320	Chlamydia trachomatis	995	63
ORF1209	688178	688732	hypothetical protein	AE001320	Chlamydia trachomatis	366	43
ORF1210	696045	696563	methyltransferase	AE001321	Chlamydia trachomatis	369	49
ORF1211	708998	708588	Glucose-1-P Adenyltransferase	AE001322	Chlamydia trachomatis	507	83
ORF1212	709808	710089	putative				
ORF1213	718240	717737	Glycerol-3-P Phosphatidyltransferase	AE001323	Chlamydia trachomatis	573	66
ORF1214	737828	737565	S19 Ribosomal Protein	AE001323	Chlamydia trachomatis	439	94

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1215	779502	780257	hypothetical protein	AE001322	Chlamydia trachomatis	476	48
ORF1216	806310	805864	hypothetical protein	AE001337	Chlamydia trachomatis	512	67
ORF1217	820931	820707	putative				
ORF1218	837696	839096	Exodeoxyribonuclease V, Gamma	AE001334	Chlamydia trachomatis	967	49
ORF1219	883307	883549	putative				
ORF1220	892010	891726	putative				
ORF1221	893277	893564	putative				
ORF1222	936998	937225	Gen. Secretion Protein E	AE001327	Chlamydia trachomatis	256	67
ORF1223	946865	947419	putative				
ORF1224	975187	975411	SWF/SNF family helicase	AE001341	Chlamydia trachomatis	363	96
ORF1225	985882	985517	hypothetical protein	AE001342	Chlamydia trachomatis	166	33
ORF1226	987713	987180	hypothetical protein	AE001342	Chlamydia trachomatis	447	59
ORF1227	988215	987733	Flagellar M-Ring Protein	AE001342	Chlamydia trachomatis	304	44
ORF1228	988754	988530	Flagellar M-Ring Protein	AE001342	Chlamydia trachomatis	92	36
ORF1229	992542	992841	hypothetical protein	AE001343	Chlamydia trachomatis	112	39
ORF1230	992759	993067	hypothetical protein	AE001343	Chlamydia trachomatis	100	32
ORF1231	1004247	1004528	D-Ala/Gly Permease	AE001344	Chlamydia trachomatis	283	64
ORF1232	1015013	1014294	235aa long hypothetical protein	AB009472	Pyrococcus horikoshii	104	54
ORF1233	1056147	1056545	putative				
ORF1234	1077682	1078035	predicted disulfide bond isomerase	AE001351	Chlamydia trachomatis	233	46
ORF1235	1088121	1088381	putative				
ORF1236	1098430	1098852	Predicted Kinase	AE001352	Chlamydia trachomatis	384	59
ORF1237	1098798	1099319	Predicted Kinase	AE001352	Chlamydia trachomatis	322	45
ORF1238	1123198	1123515	Transport Permease	AE001354	Chlamydia trachomatis	313	72
ORF1239	1123606	1124256	Tyrosine Transport	AE001354	Chlamydia trachomatis	577	58
ORF1240	1124453	1124797	Tyrosine Transport	AE001354	Chlamydia trachomatis	323	50
ORF1241	1129253	1129567	putative				
ORF1242	1164947	1164474	hypothetical protein	AE001357	Chlamydia trachomatis	412	56
ORF1243	1170457	1170053	hypothetical protein	AE001358	Chlamydia trachomatis	283	59
ORF1244	1172342	1171863	ABC transporter permease	AE001358	Chlamydia trachomatis	457	55
ORF1245	1192155	1192835	putative				
ORF1246	1192759	1192992	putative				
ORF1247	1193861	1194142	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1248	1194036	1193779	(D-Amino Acid Dehydrogenase)	AE001311	*Chlamydia trachomatis*	269	79
ORF1249	1209748	1209053	conserved hypothetical protein	AE000958	*Archaeoglobus fulgidus*	121	38
ORF1250	1215111	1215419	putative				
ORF1251	1216302	1216538	putative				
ORF1252	1228072	1227818	hypothetical protein	AE001306	*Chlamydia trachomatis*	134	39
ORF1253	1228304	1228080	xseB	AL021897	*Mycobacterium tuberculosis*	89	33
ORF1254	26599	26222	putative				
ORF1255	27609	27367	putative				
ORF1256	67206	66967	putative				
ORF1257	70612	70352	putative				
ORF1258	132703	132945	putative				
ORF1259	178073	178393	putative				
ORF1260	208576	208349	putative				
ORF1261	209156	208929	putative				
ORF1262	209263	209024	putative				
ORF1263	210304	210639	putative				
ORF1264	299009	299452	putative				
ORF1265	352106	351717	putative				
ORF1266	420182	419949	Flagellar Secretion Protein	AE001280	*Chlamydia trachomatis*	115	43
ORF1267	553602	553381	putative				
ORF1268	556538	556807	putative				
ORF1269	594348	593797	putative				
ORF1270	595169	594876	putative				
ORF1271	662148	662381	putative				
ORF1272	706528	706893	putative				
ORF1273	803315	803650	putative				
ORF1274	849551	849306	putative				
ORF1275	913676	913275	putative				
ORF1276	927087	926836	putative				
ORF1277	930587	930360	putative				
ORF1278	986531	986764	ORF 12	M72718	*Bacillus subtilis*	106	48
ORF1279	996229	996486	putative				
ORF1280	1000373	1000002	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1281	1010291	1010037	putative				
ORF1282	1011128	1010793	106aa long hypothetical protein	AB009472	Pyrococcus horikoshii	159	50
ORF1283	1012924	1012694	putative				
ORF1284	1028659	1028913	putative				
ORF1285	1086481	1086762	putative				
ORF1286	1118658	1118879	Phosphoglucomutase	AE001354	Chlamydia trachomatis	291	84
ORF1287	1170098	1169835	hypothetical protein	AE001358	Chlamydia trachomatis	187	53
ORF1288	1180828	1181184	putative				
ORF1289	1182658	1183035	putative				
ORF1290	1195076	1194795	putative				
ORF1291	1195890	1196183	putative				

Table 2

ORF Nos	begin	end	potential start
2	42	794	42
3	1258	1614	1261
4	1807	2418	1807
5	3393	2491	3393
6	3639	4067	3639
7	5649	4270	5649
8	7463	6012	7463
9	8051	8962	8051
10	9129	9959	9138
11	10687	10361	10639
12	10927	11232	10927
13	11246	12727	11246
14	12691	14190	12691
15	14484	17249	14484
16	16039	15770	16036
17	17845	20853	17845
18	21137	22042	21137
19	22046	23476	22046
20	23681	26110	23681
21	26109	25861	26109
22	26241	26978	26241
23	26960	27754	26960
24	27747	28577	27747
25	28887	29492	28950
26	29432	30028	29432
27	30024	31472	30024
28	31758	32288	31758
29	32201	33991	32201
30	33852	34541	33852
31	34783	36063	34783
32	36009	37529	36009
33	37881	39362	37881
34	39418	39161	39418

ORF Nos	begin	end	potential start
35	39366	40715	39366
36	43076	41094	43076
37	43800	43066	43800
38	44828	43785	44768
39	45340	44753	45340
40	45752	45372	45752
41	46996	45701	46996
42	47961	47569	47961
43	48960	48040	48960
44	51452	50133	51452
45	52606	51335	52606
46	53684	53319	53684
47	54195	53746	54195
48	55278	56453	55278
49	56493	57266	56493
50	57297	58526	57297
51	59851	58565	59851
52	61495	59924	61495
53	61324	62151	61324
54	62132	62470	62132
55	62474	63733	62474
56	63881	64186	63881
57	64611	64318	64611
58	65485	64673	65485
59	65999	65301	65999
60	66244	67281	66244
61	67265	67699	67265
62	67703	68539	67760
63	68805	70736	68805
64	69172	68831	69172
65	70642	71142	70642
66	71325	72029	71325
67	72060	73637	72060
68	74061	76175	74061

138

ORF Nos	begin	end	potential start
69	78351	77680	78351
70	79356	78355	79356
71	79983	79693	79983
72	80441	79938	80441
73	80475	80969	80475
74	81296	83080	81332
75	83291	83932	83291
76	84005	84769	84005
77	84975	85244	84975
78	85123	85425	85123
79	85397	85903	85397
80	85909	86583	85909
81	86626	88065	86626
82	89257	91026	89257
83	91291	93030	91291
84	93295	94086	93295
85	95285	94707	95279
86	95667	96557	95667
87	96317	97456	96317
88	98435	97968	98435
89	99460	98426	99460
90	100144	101325	100144
91	101457	101720	101457
92	101704	102273	101704
93	102356	102805	102356
94	102835	103530	102835
95	103549	104058	103549
96	104096	104491	104096
97	104601	108386	104601
98	108401	112054	108401
99	112033	112590	112033
100	112672	113682	112672
101	113726	114121	113726
102	114711	114136	114711

139

ORF Nos	begin	end	potential start
103	115267	115755	115267
104	115911	116543	115911
105	116736	118055	116778
106	117968	118522	117968
107	118530	119843	118530
108	119816	120457	119816
109	120451	122430	120451
110	122504	122950	122504
111	123528	126347	123528
112	126332	129166	126332
113	134690	129213	134690
114	134925	136382	134931
115	137870	136482	137867
116	137899	138240	137899
117	138239	137928	138239
118	139558	138257	139558
119	140352	139516	140352
120	140498	141841	140498
121	141855	142658	141855
122	144258	143050	144258
123	145258	144494	145258
124	145454	146749	145454
125	147318	146767	147318
126	148261	147677	148261
127	149029	152157	149029
128	154108	152201	154108
129	155135	154308	155135
130	155141	155467	155141
131	155703	156779	155703
132	156748	157635	156748
133	157653	158996	157653
134	159363	159986	159363
135	159880	160446	159880
136	160477	160839	160477

ORF Nos	begin	end	potential start
137	160898	161539	160898
138	161527	162153	161527
139	162144	162443	162144
140	162437	164098	162437
141	165451	164228	165451
142	166349	165411	166349
143	166949	168442	166949
144	169416	171029	169416
145	170857	171459	170857
146	172652	173428	172652
147	174626	173439	174626
148	174816	175613	174816
149	175598	175954	175598
150	175958	176935	175958
151	177708	176938	177708
152	177128	177376	177128
153	179472	177841	179472
154	179822	179517	179822
155	181793	179943	181793
156	182628	181876	182628
157	184420	183074	184420
158	184988	184467	184988
159	185483	185112	185483
160	185902	185483	185902
161	186174	185839	186174
162	187720	186587	187720
163	188318	190933	188318
164	191090	191635	191090
165	191547	192743	191547
166	192969	193469	192969
167	194044	193610	194044
168	194196	195809	194196
169	196088	198073	196088
170	198132	199454	198132

ORF Nos	begin	end	potential start
171	199351	202818	199351
172	204552	202999	204552
173	205648	204692	205639
174	205807	207327	205807
175	207182	207775	207182
176	207779	208267	207779
177	208267	209577	208267
178	211807	211271	211807
179	212188	211844	212188
180	214079	212448	214079
181	214907	214083	214907
182	216154	215429	216154
183	216115	216678	216115
184	216728	217282	216728
185	217267	217866	217267
186	218593	218261	218590
187	219821	218994	219821
188	221382	220309	221382
189	222719	221433	222719
190	223521	222724	223521
191	224499	225008	224499
192	225140	225559	225140
193	225555	226802	225555
194	227800	226892	227743
195	228335	228072	228335
196	229251	228643	229251
197	230983	229622	230983
198	231483	230983	231483
199	232063	231509	232063
200	232739	232053	232739
201	233166	234356	233166
202	233518	233165	233518
203	234536	235186	234536
204	235379	236689	235379

142

ORF Nos	begin	end	potential start
205	236680	237618	236689
206	237521	238345	237521
207	238281	238973	238281
208	238871	240115	238871
209	240191	241564	240191
210	242281	241604	242281
211	242933	242274	242933
212	243416	242976	243416
213	243500	244531	243500
214	244480	246021	244480
215	246330	247811	246330
216	247831	249174	247870
217	249437	251038	249455
218	251325	252212	251325
219	253156	254007	253156
220	253974	254852	253974
221	255258	256094	255258
222	256640	257455	256640
223	257502	258239	257502
224	257869	257501	257869
225	259248	260897	259248
226	262753	261788	262753
227	263059	262757	263059
228	264375	263182	264375
229	265985	264747	265985
230	266637	266059	266637
231	267338	266538	267338
232	267922	267473	267922
233	269647	270771	269647
234	272777	273145	272777
235	273253	273636	273253
236	273705	273977	273705
237	276016	275717	276016
238	276439	276020	276418

ORF Nos	begin	end	potential start
239	276792	277253	276792
240	277318	277599	277318
241	278578	277877	278578
242	279258	278554	279258
243	280435	279533	280435
244	281547	280849	281547
245	281696	282325	281717
246	282459	284069	282459
247	284056	284517	284056
248	284606	285775	284606
249	285592	285987	285592
250	286179	286976	286179
251	287583	287002	287583
252	287951	287451	287951
253	288499	288816	288499
254	289674	288505	289674
255	288839	289213	288839
256	289970	290254	289970
257	291931	292803	291931
258	293258	292755	293258
259	293718	293272	293718
260	294630	293953	294630
261	296153	294636	296153
262	294817	295068	294817
263	296354	297862	296354
264	298415	297879	298415
265	298777	298253	298777
266	299572	298781	299572
267	300487	299633	300487
268	301586	300702	301568
269	302440	301571	302440
270	302838	302437	302838
271	303335	302745	303335
272	304394	303852	304394

ORF Nos	begin	end	potential start
273	304606	305223	304606
274	305394	306236	305394
275	306501	307439	306501
276	308033	307458	308033
277	308924	308037	308924
278	309485	310180	309485
279	310426	311214	310426
280	311597	311253	311504
281	312772	311780	312772
282	313425	312772	313425
283	313646	313377	313646
284	313937	314665	313937
285	315576	314755	315576
286	316157	315531	316157
287	318657	316156	318657
288	321042	318676	321042
289	321445	321098	321445
290	322309	321710	322309
291	323190	322366	323181
292	323843	323181	323843
293	324878	323856	324878
294	325340	326410	325340
295	326433	327836	326433
296	328465	327839	328465
297	329360	328857	329360
298	330907	329357	330907
299	332455	330956	332455
300	334536	332395	334536
301	336091	334877	336091
302	336103	337302	336103
303	338129	338830	338129
304	338965	339501	338965
305	339508	340143	339508
306	340247	342967	340247

ORF Nos	begin	end	potential start
307	343385	343810	343385
308	344171	343935	344171
309	345082	344330	345073
310	346005	345082	346005
311	346784	346437	346784
312	347029	346715	347029
313	347034	347723	347034
314	348075	350459	348075
315	350598	351071	350598
316	351075	352175	351096
317	353291	352230	353267
318	353442	354467	353442
319	354451	354933	354451
320	355000	355449	355000
321	355448	356743	355448
322	355953	355642	355953
323	359310	356827	359310
324	359120	359377	359120
325	359525	359908	359525
326	361290	359947	361290
327	363785	361362	363746
328	364496	363888	364496
329	364832	365290	364832
330	365304	365669	365304
331	366599	365667	366599
332	367291	369030	367291
333	369134	369808	369134
334	369917	370438	369917
335	370365	372647	370365
336	372557	373066	372557
337	373020	373442	373020
338	373467	374195	373467
339	374176	375099	374176
340	375676	375083	375676

ORF Nos	begin	end	potential start
341	376173	375634	376173
342	376564	377643	376564
343	377956	379773	377956
344	379781	380425	379805
345	380281	381000	380281
346	381008	381460	381008
347	381460	383037	381460
348	383257	383523	383257
349	383553	385304	383553
350	385397	386458	385400
351	387242	386514	387242
352	388764	387013	388764
353	390120	390932	390120
354	390919	391818	390961
355	392379	391885	392379
356	392582	392986	392582
357	392776	393684	392776
358	394151	394804	394151
359	394928	395308	394928
360	395259	395990	395259
361	397815	395953	397815
362	398850	397831	398850
363	400085	399099	400085
364	401245	400073	401236
365	401474	401136	401474
366	402199	401423	402199
367	403193	402186	403166
368	403650	404165	403650
369	404343	405914	404343
370	405984	407327	405984
371	407712	408806	407712
372	410439	409075	410439
373	411826	410954	411826
374	412482	414302	412482

ORF Nos	begin	end	potential start
375	415402	414407	415402
376	415848	415237	415848
377	417131	415866	417131
378	417258	417566	417258
379	418326	417454	418326
380	420057	418426	420057
381	420448	420720	420448
382	420980	421552	420980
383	421556	422029	421556
384	422461	422925	422461
385	423562	424320	423562
386	424250	424591	424250
387	424830	426047	424830
388	426240	427397	426240
389	428841	430703	428841
390	430694	431446	430694
391	431597	432100	431597
392	432165	432779	432165
393	433272	432832	433272
394	433925	433227	433922
395	436678	433934	436678
396	437176	438357	437176
397	440317	438518	440317
398	440001	440345	440001
399	441233	440517	441233
400	440719	441012	440719
401	442192	441230	442192
402	442888	442343	442888
403	442371	442961	442371
404	443578	443003	443578
405	444500	443526	444500
406	444842	444528	444842
407	445009	444743	445009
408	445718	445182	445718

ORF Nos	begin	end	potential start
409	445807	447804	445807
410	448738	447803	448738
411	449628	448618	449628
412	450298	450867	450298
413	450713	451207	450713
414	451211	452452	451211
415	452448	453659	452448
416	454843	453725	454843
417	455608	454865	455608
418	456243	457007	456243
419	457016	457708	457016
420	458368	457979	458368
421	459496	458372	459496
422	459493	460194	459493
423	461446	460355	461446
424	462298	461450	462298
425	462444	463349	462444
426	464241	463342	464241
427	464574	465065	464574
428	465129	465611	465129
429	465571	466317	465571
430	466317	467093	466317
431	466999	467502	466999
432	469691	467715	469691
433	470691	469660	470691
434	472010	470709	472010
435	471545	471799	471545
436	472359	472045	472359
437	473523	472732	473523
438	474889	473441	474889
439	477323	475365	477323
440	478496	477597	478496
441	478722	479273	478722
442	479277	479705	479277

ORF Nos	begin	end	potential start
443	480050	481450	480050
444	481469	482053	481469
445	482600	482025	482600
446	482654	484204	482654
447	484211	485170	484211
448	485170	485838	485170
449	485813	486580	485813
450	486976	486638	486976
451	489071	487764	489071
452	489341	489090	489341
453	489958	489152	489958
454	490549	489962	490549
455	491163	490522	491163
456	491396	491112	491396
457	492121	491390	492121
458	492304	494838	492304
459	495943	494822	495943
460	496011	496565	496170
461	496569	497228	496569
462	497358	497834	497358
463	497770	498327	497770
464	499209	499589	499209
465	499520	499792	499520
466	500774	504169	500774
467	504139	504600	504139
468	504865	506877	504865
469	506790	507671	506790
470	507718	510507	507718
471	508325	507912	508325
472	510660	513440	510660
473	514965	513787	514920
474	517347	515419	517347
475	517058	517363	517058
476	517798	517277	517798

ORF Nos	begin	end	potential start
477	518200	517847	518200
478	518300	521146	518363
479	521392	522948	521407
480	523244	524809	523322
481	524379	524125	524379
482	524649	526238	524649
483	526265	527104	526268
484	526947	526702	526947
485	526975	528450	526975
486	528408	529199	528408
487	530612	529542	530612
488	531656	530616	531656
489	533974	532067	533974
490	536432	534324	536432
491	537150	536707	537150
492	537928	537080	537928
493	538438	537932	538438
494	538737	538333	538737
495	539594	539127	539594
496	541215	539590	541215
497	542571	541282	542571
498	543014	542457	543014
499	543369	542962	543369
500	543809	546628	543815
501	546619	549525	546619
502	547293	546994	547293
503	549699	550523	549699
504	550490	551551	550490
505	551448	552623	551448
506	552652	555117	552652
507	555029	555493	555029
508	558006	555673	558006
509	559694	558162	559694
510	558208	558573	558208

ORF Nos	begin	end	potential start
511	561692	559899	561692
512	561412	561708	561412
513	563942	561777	563942
514	564969	563950	564969
515	566204	564936	566198
516	567717	566302	567717
517	568526	567708	568526
518	569467	568742	569467
519	571065	569431	571065
520	571828	571118	571783
521	572202	573308	572202
522	573146	575056	573146
523	575023	575916	575023
524	577891	576497	577891
525	578914	578204	578914
526	579924	578857	579924
527	580187	579858	580187
528	580017	580406	580017
529	581086	580187	581086
530	581367	581828	581367
531	581678	582367	581678
532	582361	583428	582361
533	584690	583431	584690
534	585237	584950	585237
535	585626	586888	585626
536	586846	587907	586888
537	589049	588180	589049
538	590500	589301	590455
539	590755	592458	590755
540	592526	592903	592526
541	592836	593747	592836
542	593747	594298	593747
543	594331	595947	594331
544	595905	596309	595905

ORF Nos	begin	end	potential start
545	596514	597215	596514
546	597184	597957	597184
547	597755	598612	597755
548	598602	599204	598602
549	599373	599939	599373
550	600903	602072	600903
551	602240	602587	602240
552	602637	603272	602637
553	603142	604512	603142
554	604627	605853	604627
555	605790	606620	605790
556	606571	607281	606571
557	609004	607355	609004
558	610906	609932	610906
559	611786	611004	611786
560	612333	611746	612333
561	613897	612341	613897
562	615179	616279	615179
563	616610	617383	616610
564	618796	617810	618796
565	620004	618826	620004
566	619649	619918	619649
567	621265	620021	621265
568	622359	621265	622359
569	623420	622560	623420
570	624297	623335	624297
571	624773	624174	624773
572	625029	625484	625029
573	625488	625883	625488
574	625892	626395	625892
575	626444	627790	626444
576	627912	628607	627930
577	628774	629697	628774
578	629660	631639	629660

ORF Nos	begin	end	potential start
579	631725	633551	631725
580	633520	636957	633520
581	637232	638098	637232
582	640648	639593	640648
583	640979	640728	640979
584	641327	641007	641327
585	641687	642283	641687
586	643023	642286	643023
587	643330	643076	643330
588	643704	643351	643704
589	645628	643676	645628
590	645783	645538	645756
591	646269	645793	646269
592	646751	646314	646751
593	647848	647045	647848
594	648393	650336	648393
595	651016	650420	651007
596	652956	651289	652956
597	653395	653126	653395
598	655740	654193	655740
599	656508	655966	656508
600	658140	657022	658140
601	660216	658525	660216
602	663238	660248	663238
603	664461	663157	664452
604	665735	664635	665735
605	666212	666994	666212
606	666998	667921	666998
607	667909	668568	667909
608	668502	669203	668502
609	669154	670893	669175
610	672226	670853	672226
611	671137	671424	671137
612	672453	673001	672453

ORF Nos	begin	end	potential start
613	673072	674721	673072
614	674549	674262	674549
615	675518	674796	675518
616	676083	675499	676083
617	676630	676067	676630
618	677016	676600	677016
619	677647	677015	677647
620	677990	678259	677990
621	679444	680097	679444
622	680097	680897	680097
623	681637	680849	681637
624	681409	682281	681409
625	682453	682821	682453
626	682763	683902	682763
627	684616	683969	684616
628	685169	684534	685169
629	685986	685117	685986
630	686278	687288	686278
631	687483	688151	687483
632	688740	689501	688740
633	690242	689622	690242
634	690470	691126	690470
635	692600	691497	692600
636	692674	695064	692674
637	695049	696032	695064
638	697964	696585	697964
639	699803	698274	699803
640	701926	699788	701926
641	703196	702567	703196
642	704221	703208	704221
643	704240	705289	704240
644	706070	705300	706070
645	706841	706254	706838
646	707596	706811	707596

ORF Nos	begin	end	potential start
647	708666	707677	708666
648	709793	709119	709793
649	711523	710132	711523
650	712236	711523	712236
651	714734	712125	714734
652	715759	714761	715759
653	717538	715886	717538
654	719113	720243	719113
655	720590	722422	720590
656	722406	723056	722406
657	723551	723120	723551
658	724246	723626	724246
659	724754	724251	724754
660	725868	724900	725868
661	727115	726270	727115
662	728126	727119	728126
663	728594	728208	728594
664	729614	728604	729614
665	729778	729533	729778
666	730149	729751	730149
667	730539	730174	730539
668	731983	730598	731983
669	732427	731996	732427
670	732917	732423	732917
671	733598	733320	733598
672	733869	733492	733869
673	734298	733900	734298
674	734858	734319	734858
675	735195	734863	735195
676	735578	735342	735578
677	735861	735604	735861
678	736492	736079	736492
679	737192	736524	737192
680	737555	737211	737555

ORF Nos	begin	end	potential start
681	738688	737837	738688
682	739048	738713	739048
683	739736	739065	739736
684	740477	739773	740477
685	740659	740958	740659
686	741722	740721	741722
687	742789	741827	742789
688	743618	742782	743618
689	744092	743634	744092
690	744604	744107	744604
691	744953	744498	744953
692	746608	744986	746608
693	747085	746621	747085
694	747974	747219	747974
695	748594	748169	748594
696	749145	748573	749145
697	749652	749957	749652
698	750446	749979	750446
699	751219	750446	751219
700	753042	751291	753042
701	754309	753020	754309
702	755120	756175	755120
703	756120	756485	756120
704	756499	760227	756499
705	761217	760297	761178
706	761297	761809	761330
707	761782	762282	761782
708	762260	762895	762299
709	762867	763316	762867
710	763780	763325	763780
711	763861	765168	763861
712	766809	765697	766809
713	768051	766888	768051
714	768566	768321	768566

ORF Nos	begin	end	potential start
715	769342	768551	769342
716	770532	769378	770532
717	771451	770804	771451
718	773058	771847	773058
719	773094	773456	773094
720	774376	773093	774376
721	775123	774380	775123
722	775398	774916	775398
723	775046	776077	775046
724	776070	777041	776070
725	777964	777536	777964
726	778176	777904	778176
727	778621	779334	778684
728	781173	780307	781173
729	781526	781116	781526
730	782784	781555	782784
731	783572	782805	783572
732	785032	783581	785032
733	786412	785360	786412
734	788429	786450	788429
735	788944	788528	788944
736	789758	788901	789758
737	790332	791504	790338
738	791846	792721	791846
739	792724	793569	792724
740	793580	794323	793580
741	794304	794843	794304
742	795217	795732	795217
743	795722	796795	795722
744	798735	797053	798735
745	799823	798681	799823
746	799297	799578	799297
747	801313	799808	801313
748	802453	801332	802453

ORF Nos	begin	end	potential start
749	803299	802457	803299
750	803811	803290	803811
751	805151	803826	805151
752	805860	805156	805860
753	806604	806332	806604
754	806913	806608	806913
755	808222	806903	808222
756	808751	808146	808751
757	809437	808673	809437
758	809939	809454	809939
759	811235	810213	811235
760	811779	813056	811779
761	812890	812516	812890
762	812954	813583	812954
763	813587	815023	813587
764	815420	815746	815420
765	816036	817010	816036
766	817111	817356	817111
767	817791	818609	817797
768	818609	819094	818609
769	819104	819823	819104
770	820722	819826	820722
771	822313	821000	822313
772	823503	822238	823503
773	823678	825612	823678
774	825461	826312	825461
775	827280	826645	827280
776	828604	827171	828604
777	830026	828713	830026
778	831047	830085	831047
779	831725	831051	831725
780	832220	833098	832220
781	833851	833396	833851
782	834068	835039	834068

ORF Nos	begin	end	potential start
783	835792	835127	835792
784	837624	836116	837624
785	838951	840882	838951
786	840869	842185	840869
787	841989	843455	841989
788	843242	844021	843242
789	845018	843987	844997
790	846174	844990	846174
791	848509	846311	848509
792	848568	849014	848568
793	849082	850488	849088
794	851512	850574	851512
795	852064	852447	852064
796	852398	853690	852398
797	855118	854243	855118
798	855751	855128	855751
799	856551	855829	856551
800	856730	858556	856730
801	858717	859601	858717
802	859591	860205	859591
803	861132	860284	861132
804	861426	861163	861426
805	861701	862921	861701
806	863026	864798	863026
807	864831	865256	864831
808	865226	866581	865226
809	866562	867119	866562
810	867025	867816	867025
811	867820	868497	867820
812	869743	868661	869743
813	870633	870094	870633
814	871929	870646	871929
815	872538	872086	872538
816	873908	872517	873908

ORF Nos	begin	end	potential start
817	874281	874670	874281
818	874582	875286	874582
819	877857	875377	877857
820	878446	879255	878446
821	880635	879268	880635
822	882524	880593	882524
823	882612	883319	882612
824	884155	883538	884155
825	884340	885611	884343
826	885722	887302	885722
827	887587	888153	887587
828	888627	888220	888627
829	889330	888716	889330
830	889898	889323	889898
831	891190	889898	891190
832	891828	891247	891828
833	892421	892017	892421
834	893116	892421	893116
835	892521	892925	892521
836	893392	895419	893392
837	895745	896527	895745
838	896668	897558	896668
839	897565	899442	897565
840	899420	900229	899420
841	903230	900237	903230
842	905081	903234	905081
843	906931	905045	906931
844	907248	907832	907299
845	907784	908128	907784
846	908132	908677	908132
847	908589	909320	908589
848	909405	911465	909405
849	911677	912360	911725
850	912303	912821	912303

ORF Nos	begin	end	potential start
851	912937	913983	912937
852	915128	914067	915128
853	916658	915303	916658
854	915627	915376	915627
855	917707	916853	917707
856	918837	917722	918837
857	919868	918837	919868
858	920434	919880	920434
859	921187	920438	921187
860	921959	921195	921959
861	923773	921995	923773
862	922146	922415	922146
863	923943	923674	923943
864	924077	925006	924077
865	925436	925083	925436
866	926524	925349	926524
867	927920	926433	927920
868	928319	927951	928319
869	928963	928334	928963
870	929248	930987	929248
871	930995	932059	930995
872	932121	933515	932175
873	932881	932513	932881
874	933485	935746	933485
875	935724	937082	935724
876	937229	938410	937229
877	938281	938805	938281
878	938809	939255	938824
879	939165	939782	939165
880	939760	940791	939790
881	940822	941106	940822
882	940977	941351	940977
883	942537	941623	942429
884	942784	942500	942763

ORF Nos	begin	end	potential start
885	943149	942799	943149
886	943799	943029	943799
887	944055	943732	944055
888	944413	943994	944404
889	945395	944556	945395
890	945853	945389	945853
891	946392	945751	946392
892	947410	948081	947431
893	949871	948915	949871
894	951058	949868	951058
895	951249	950959	951249
896	951664	952134	951664
897	952674	952165	952674
898	953491	952589	953491
899	955324	953495	955324
900	955823	955281	955823
901	957082	955847	957082
902	957902	957270	957902
903	959231	957906	959231
904	959376	960284	959376
905	960266	961669	960347
906	961856	964765	961856
907	966855	965395	966855
908	968204	966975	968204
909	968791	968237	968791
910	969498	968731	969498
911	969858	969511	969858
912	970118	969762	970118
913	970593	970300	970593
914	971261	970542	971261
915	971680	971123	971680
916	971876	975100	971876
917	975419	976516	975419
918	976584	978320	976584

ORF Nos	begin	end	potential start
919	977680	977231	977680
920	978399	980738	978399
921	980756	981928	980756
922	982974	981931	982962
923	984120	983119	984120
924	985502	984120	985502
925	987180	985882	987180
926	987172	987444	987172
927	989846	989049	989846
928	991048	989846	991048
929	991638	990955	991638
930	991794	992498	991794
931	993619	993041	993619
932	993530	994792	993548
933	995970	994795	995970
934	996857	995739	996857
935	997603	996782	997603
936	998969	997572	998969
937	998896	1000023	998896
938	1000087	1001340	1000087
939	1001357	1001818	1001357
940	1003288	1001873	1003288
941	1003487	1004146	1003496
942	1004485	1005639	1004689
943	1005643	1005972	1005643
944	1006784	1006116	1006784
945	1007563	1006769	1007563
946	1009226	1007568	1009226
947	1009989	1009336	1009989
948	1015852	1016337	1015852
949	1016561	1016181	1016561
950	1016297	1017532	1016297
951	1016802	1016452	1016802
952	1018993	1017701	1018993

ORF Nos	begin	end	potential start
953	1019454	1019137	1019454
954	1020764	1019562	1020764
955	1021405	1021037	1021405
956	1021821	1024286	1021821
957	1024697	1024248	1024697
958	1025569	1024508	1025551
959	1026969	1025590	1026969
960	1027789	1026947	1027789
961	1031199	1027945	1031199
962	1031717	1031172	1031717
963	1033057	1031612	1033057
964	1033425	1033039	1033425
965	1033784	1033200	1033784
966	1033963	1036038	1033963
967	1036945	1036010	1036945
968	1037110	1037679	1037110
969	1037696	1037944	1037696
970	1038916	1037975	1038916
971	1040582	1039026	1040582
972	1040997	1042337	1040997
973	1042357	1043403	1042357
974	1043367	1044623	1043367
975	1044607	1045362	1044607
976	1045384	1046538	1045384
977	1046447	1047517	1046447
978	1047521	1049956	1047521
979	1050611	1050036	1050611
980	1050925	1050566	1050925
981	1051728	1051090	1051728
982	1051743	1052063	1051743
983	1052101	1053126	1052101
984	1054201	1053107	1054201
985	1054242	1055555	1054242
986	1055483	1055908	1055483

ORF Nos	begin	end	potential start
987	1056609	1056965	1056609
988	1056961	1058232	1056985
989	1058238	1058687	1058238
990	1059371	1058727	1059371
991	1059526	1060578	1059526
992	1061553	1060579	1061553
993	1061674	1062411	1061674
994	1062377	1064077	1062377
995	1064116	1065243	1064116
996	1067451	1065178	1067451
997	1068065	1067376	1068065
998	1068209	1068706	1068230
999	1069958	1068819	1069958
1000	1071163	1070033	1071163
1001	1072438	1071332	1072438
1002	1072997	1073476	1072997
1003	1074239	1075864	1074239
1004	1076790	1075867	1076790
1005	1077268	1076573	1077268
1006	1077999	1078724	1077999
1007	1079088	1078672	1079088
1008	1079642	1079944	1079642
1009	1080501	1079995	1080468
1010	1080775	1081341	1080775
1011	1083158	1081350	1083158
1012	1084677	1083235	1084677
1013	1085648	1084632	1085648
1014	1086117	1086737	1086117
1015	1086692	1087897	1086692
1016	1088646	1089005	1088646
1017	1089146	1089805	1089146
1018	1092931	1089890	1092931
1019	1093179	1092889	1093179
1020	1093584	1094204	1093584

ORF Nos	begin	end	potential start
1021	1095619	1094192	1095619
1022	1096074	1096628	1096074
1023	1096633	1097082	1096633
1024	1097266	1097601	1097266
1025	1097622	1097867	1097622
1026	1097886	1098392	1097886
1027	1099521	1099279	1099521
1028	1099689	1101053	1099704
1029	1102192	1101107	1102192
1030	1104950	1102116	1104950
1031	1106508	1104946	1106508
1032	1106722	1107249	1106722
1033	1107463	1108101	1107463
1034	1108041	1108421	1108041
1035	1108520	1113370	1108520
1036	1114958	1113447	1114958
1037	1116915	1115071	1116915
1038	1118183	1116894	1118183
1039	1118846	1120030	1118846
1040	1120040	1120522	1120040
1041	1120510	1121430	1120510
1042	1121321	1121866	1121321
1043	1122123	1122899	1122123
1044	1124842	1125564	1124842
1045	1126526	1125579	1126526
1046	1126519	1127676	1126519
1047	1127672	1128571	1127672
1048	1130230	1131336	1130230
1049	1131480	1132553	1131480
1050	1132830	1133843	1132830
1051	1134121	1134855	1134121
1052	1134642	1135592	1134642
1053	1135964	1135653	1135964
1054	1137132	1135954	1137132

ORF Nos	begin	end	potential start
1055	1137169	1140102	1137169
1056	1141365	1140112	1141344
1057	1142150	1141356	1142150
1058	1142520	1145660	1142520
1059	1145627	1146721	1145627
1060	1146862	1147545	1146862
1061	1147666	1148190	1147666
1062	1148514	1148224	1148514
1063	1149136	1148348	1149136
1064	1149702	1149166	1149702
1065	1150031	1150591	1150031
1066	1150785	1151147	1150785
1067	1151165	1152181	1151165
1068	1152522	1154591	1152522
1069	1155666	1154566	1155666
1070	1156743	1155670	1156740
1071	1156859	1157815	1156859
1072	1157982	1160735	1157982
1073	1162620	1160917	1162620
1074	1162970	1162590	1162970
1075	1163532	1164020	1163532
1076	1163995	1164294	1163995
1077	1165569	1165030	1165569
1078	1166108	1165566	1166108
1079	1166644	1166141	1166644
1080	1167055	1168374	1167055
1081	1169218	1168337	1169218
1082	1169823	1169218	1169823
1083	1171324	1170572	1171324
1084	1172085	1171177	1172085
1085	1172394	1173773	1172394
1086	1175209	1173881	1175209
1087	1175555	1175127	1175360
1088	1175778	1177043	1175778

ORF Nos	begin	end	potential start
1089	1177177	1179048	1177177
1090	1179156	1180085	1179156
1091	1180045	1180779	1180045
1092	1181942	1180788	1181942
1093	1182296	1181961	1182296
1094	1183844	1182300	1183844
1095	1184420	1183848	1184420
1096	1185382	1184366	1185382
1097	1185858	1185226	1185858
1098	1186164	1186481	1186185
1099	1187386	1186484	1187386
1100	1187370	1189028	1187370
1101	1189321	1190889	1189321
1102	1191142	1192146	1191142
1103	1191974	1191729	1191974
1104	1193815	1192991	1193815
1105	1195702	1194248	1195702
1106	1196303	1195716	1196303
1107	1196831	1196337	1196831
1108	1197807	1196746	1197651
1109	1198740	1197883	1198668
1110	1200232	1198721	1200232
1111	1201286	1200135	1201286
1112	1202386	1201259	1202350
1113	1202901	1202350	1202901
1114	1204162	1202816	1204162
1115	1203177	1203464	1203177
1116	1205028	1204180	1205028
1117	1206392	1204878	1206392
1118	1206742	1206086	1206742
1119	1207872	1206724	1207872
1120	1208852	1207851	1208852
1121	1210518	1209742	1210518
1122	1210703	1211494	1210703

ORF Nos	begin	end	potential start
1123	1211870	1212754	1211870
1124	1212742	1214064	1212742
1125	1214046	1214858	1214046
1126	1215551	1216318	1215551
1127	1216493	1216849	1216493
1128	1217183	1219612	1217183
1129	1220068	1219673	1220068
1130	1219710	1220669	1219710
1131	1220630	1221376	1220630
1132	1221645	1223681	1221645
1133	1223894	1224988	1223900
1134	1225000	1225830	1225000
1135	1227810	1225879	1227810
1136	1226528	1226908	1226528
1137	1229972	1228311	1229972
1138	47569	47018	47569
1139	49980	49117	49980
1140	53356	52898	53356
1141	54477	54884	54477
1142	63753	63998	63753
1143	77164	77487	77164
1144	79724	79302	79724
1145	88721	88951	88721
1146	94067	94429	94067
1147	122832	123341	122832
1148	147536	147234	147536
1149	158990	159346	158990
1150	168470	168979	168470
1151	169183	169452	169204
1152	171785	171504	171785
1153	172518	171775	172518
1154	193599	194045	193599
1155	195704	196075	195704
1156	210687	210145	210684

ORF Nos	begin	end	potential start
1157	211100	210708	211100
1158	215420	215088	215420
1159	217914	218246	217914
1160	218925	218701	218925
1161	223785	223525	223785
1162	224271	223999	224271
1163	228691	228407	228691
1164	235050	235334	235050
1165	252308	253021	252308
1166	258280	258912	258280
1167	261325	261567	261325
1168	268195	268878	268195
1169	269447	268881	269447
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1186	407379	407621	407379
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1189	428172	428486	428172
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ORF Nos	begin	end	potential start
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1196	499795	500466	499795
1197	571928	572344	571928
1198	572367	572131	572367
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1201	609731	608895	609731
1202	614039	614755	614039
1203	614823	615152	614823
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1205	638819	639094	638819
1206	639073	639636	639073
1207	647901	648236	647901
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1213	718240	717737	718240
1214	737828	737565	737828
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1217	820931	820707	820931
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1220	892010	891726	892010
1221	893277	893564	893277
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1223	946865	947419	946865
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ORF Nos	begin	end	potential start
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1231	1004247	1004528	1004268
1232	1015013	1014294	1015013
1233	1056147	1056545	1056147
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1235	1088121	1088381	1088121
1236	1098430	1098852	1098430
1237	1098798	1099319	1098798
1238	1123198	1123515	1123198
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1240	1124453	1124797	1124453
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1242	1164947	1164474	1164947
1243	1170457	1170053	1170457
1244	1172342	1171863	1172342
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1246	1192759	1192992	1192759
1247	1193861	1194142	1193861
1248	1194036	1193779	1194036
1249	1209748	1209053	1209748
1250	1215111	1215419	1215111
1251	1216302	1216538	1216302
1252	1228072	1227818	1228072
1253	1228304	1228080	1228304
1254	26599	26222	26599
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1256	67206	66967	67197
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ORF Nos	begin	end	potential start
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1261	209156	208929	209156
1262	209263	209024	209263
1263	210304	210639	210304
1264	299009	299452	299030
1265	352106	351717	352061
1266	420182	419949	420170
1267	553602	553381	553602
1268	556538	556807	556538
1269	594348	593797	594342
1270	595169	594876	595160
1271	662148	662381	662160
1272	706528	706893	706528
1273	803315	803650	803339
1274	849551	849306	849551
1275	913676	913275	913676
1276	927087	926836	927087
1277	930587	930360	930587
1278	986531	986764	986531
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1283	1012924	1012694	1012924
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1285	1086481	1086762	1086481
1286	1118658	1118879	1118658
1287	1170098	1169835	1170098
1288	1180828	1181184	1180828
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1291	1195890	1196183	1195890
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ORF Nos	begin	end	potential start
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1297	377646	378068	377646

Table 4

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TABLE 5

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1296	F	1588	3016	F	835834	4736	B	458008
1297	F	1229711	3017	F	833938	4737	B	459836
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1299	F	369	3019	F	835536	4739	B	460488
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1303	F	2126	3023	F	838723	4743	B	462365
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1305	F	3843	3025	F	839825	4745	B	463286
1306	F	7832	3026	F	842960	4746	B	461680
1307	F	5909	3027	F	841123	4747	B	463584
1308	F	8887	3028	F	843765	4748	B	462520
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1310	F	10139	3030	F	844768	4750	B	463584
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1313	F	8799	3033	F	844175	4753	B	466398
1314	F	10997	3034	F	848293	4754	B	465288
1315	F	9037	3035	F	846449	4755	B	467243
1316	F	12458	3036	F	848867	4756	B	465835
1317	F	10572	3037	F	846964	4757	B	467738
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1319	F	12365	3039	F	848426	4759	B	468474
1320	F	15529	3040	F	851788	4760	B	467322
1321	F	13629	3041	F	849899	4761	B	469217
1322	F	17626	3042	F	852166	4762	B	467738
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1328	F	23462	3048	F	855595	4768	B	472075
1329	F	21557	3049	F	853679	4769	B	473922
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1336	F	27528	3056	F	860050	4776	B	475116
1337	F	25628	3057	F	858116	4777	B	477009
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1382	F	51088	3102	F	884035	4822	B	495083
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1385	F	50721	3105	F	883599	4825	B	498063
1386	F	53065	3106	F	887340	4826	B	496789
1387	F	51176	3107	F	885448	4827	B	498688
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1391	F	52351	3111	F	886570	4831	B	499966
1392	F	55058	3112	F	889100	4832	B	498552
1393	F	53159	3113	F	887201	4833	B	500508
1394	F	56274	3114	F	889655	4834	B	499240

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1397	F	55156	3117	F	889105	4837	B	501762
1398	F	58343	3118	F	891504	4838	B	500020
1399	F	56392	3119	F	889593	4839	B	501915
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1401	F	59177	3121	F	889841	4841	B	502628
1402	F	59701	3122	F	892279	4842	B	504395
1403	F	57802	3123	F	890400	4843	B	506292
1404	F	61887	3124	F	892182	4844	B	504885
1405	F	59971	3125	F	890288	4845	B	506772
1406	F	62255	3126	F	893010	4846	B	507107
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1416	F	65072	3136	F	899197	4856	B	515276
1417	F	63140	3137	F	897279	4857	B	517040
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1421	F	65146	3141	F	901103	4861	B	519510
1422	F	67466	3142	F	904798	4862	B	518075
1423	F	65580	3143	F	902923	4863	B	519947
1424	F	68569	3144	F	906993	4864	B	518429
1425	F	66686	3145	F	905129	4865	B	520326
1426	F	68609	3146	F	907564	4866	B	521416
1427	F	66688	3147	F	905665	4867	B	523319
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1433	F	69935	3153	F	907286	4873	B	526501
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1462	F	85690	3182	F	923428	4902	B	541474
1463	F	83790	3183	F	921546	4903	B	543411
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1468	F	89038	3188	F	925102	4908	B	543608
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1474	F	93846	3194	F	928112	4914	B	547523
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1477	F	92561	3197	F	927129	4917	B	552702
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1481	F	94197	3201	F	929987	4921	B	554756
1482	F	97706	3202	F	932291	4922	B	555340
1483	F	95841	3203	F	930323	4923	B	557240
1484	F	98142	3204	F	933264	4924	B	555736
1485	F	96292	3205	F	931339	4925	B	557619
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1487	F	98011	3207	F	933605	4927	B	560135
1488	F	101229	3208	F	936779	4928	B	558821
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1491	F	99552	3211	F	935108	4931	B	561816
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1493	F	100237	3213	F	936162	4933	B	563858
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1498	F	103877	3218	F	939541	4938	B	565229
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1502	F	108182	3222	F	940758	4942	B	567974
1503	F	106280	3223	F	938826	4943	B	569872
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1505	F	109911	3225	F	939470	4945	B	570655
1506	F	112412	3226	F	942261	4946	B	569707
1507	F	110553	3227	F	940373	4947	B	571605
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1509	F	111571	3229	F	940654	4949	B	573207
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1512	F	114990	3232	F	943510	4952	B	572628
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1527	F	120382	3247	F	946774	4967	B	582047
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1538	F	136249	3258	F	953230	4978	B	583651
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1562	F	147455	3282	F	969289	5002	B	596170
1563	F	145501	3283	F	967389	5003	B	598096
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1567	F	150062	3287	F	968137	5007	B	599365
1568	F	154064	3288	F	970317	5008	B	598191
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1587	F	158778	3307	F	979785	5027	B	608046
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1599	F	164828	3319	F	985049	5039	B	613917
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1602	F	168907	3322	F	988307	5042	B	614136
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1614	F	173217	3334	F	992522	5054	B	620142
1615	F	171316	3335	F	990640	5055	B	622052
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1617	F	172680	3337	F	991361	5057	B	622124
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1626	F	177608	3346	F	997317	5066	B	625020
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1628	F	179259	3348	F	998653	5068	B	625774
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1637	F	182335	3357	F	1001317	5077	B	630730
1638	F	184870	3358	F	1004049	5078	B	629982
1639	F	182962	3359	F	1002132	5079	B	631822

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1643	F	183685	3363	F	1003518	5083	B	635675
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1657	F	191474	3377	F	1014172	5097	B	643106
1658	F	193977	3378	F	1015924	5098	B	641605
1659	F	192059	3379	F	1014059	5099	B	643503
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1661	F	193585	3381	F	1014330	5101	B	644407
1662	F	195868	3382	F	1017479	5102	B	643243
1663	F	193969	3383	F	1015558	5103	B	645145
1664	F	197913	3384	F	1018915	5104	B	643550
1665	F	196013	3385	F	1017003	5105	B	645450
1666	F	199088	3386	F	1019328	5106	B	643925
1667	F	197213	3387	F	1017440	5107	B	645837
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1669	F	200876	3389	F	1018915	5109	B	647759
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1671	F	202497	3391	F	1019671	5111	B	647969
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1673	F	203664	3393	F	1022107	5113	B	648429
1674	F	206940	3394	F	1024277	5114	B	646973

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1676	F	207560	3396	F	1025368	5116	B	648115
1677	F	205587	3397	F	1023468	5117	B	650007
1678	F	208048	3398	F	1026671	5118	B	648516
1679	F	206139	3399	F	1024821	5119	B	650374
1680	F	209923	3400	F	1027688	5120	B	650567
1681	F	208023	3401	F	1025823	5121	B	652472
1682	F	210455	3402	F	1030916	5122	B	651251
1683	F	208569	3403	F	1029047	5123	B	653140
1684	F	211049	3404	F	1031342	5124	B	653186
1685	F	209147	3405	F	1029430	5125	B	655076
1686	F	211596	3406	F	1032795	5126	B	653628
1687	F	209705	3407	F	1030916	5127	B	655515
1688	F	212226	3408	F	1032978	5128	B	656010
1689	F	210311	3409	F	1031078	5129	B	657870
1690	F	213832	3410	F	1033730	5130	B	656761
1691	F	211960	3411	F	1031839	5131	B	658636
1692	F	214866	3412	F	1035774	5132	B	658389
1693	F	212921	3413	F	1033821	5133	B	660295
1694	F	215173	3414	F	1036884	5134	B	660436
1695	F	213307	3415	F	1034954	5135	B	662352
1696	F	215800	3416	F	1037476	5136	B	663483
1697	F	213957	3417	F	1035577	5137	B	665358
1698	F	216489	3418	F	1037714	5138	B	664701
1699	F	214549	3419	F	1035847	5139	B	666607
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1701	F	215100	3421	F	1036884	5141	B	667856
1702	F	217665	3422	F	1040777	5142	B	667238
1703	F	215793	3423	F	1038856	5143	B	669172
1704	F	218039	3424	F	1042132	5144	B	668195
1705	F	216071	3425	F	1040216	5145	B	670046
1706	F	218476	3426	F	1043148	5146	B	668791
1707	F	216560	3427	F	1041215	5147	B	670691
1708	F	218769	3428	F	1044388	5148	B	669426
1709	F	216809	3429	F	1042445	5149	B	671326

1710	F	220020	3430	F	1045164	5150	B	671116
1711	F	218128	3431	F	1043224	5151	B	673055
1712	F	221210	3432	F	1046223	5152	B	671659
1713	F	219275	3433	F	1044324	5153	B	673547
1714	F	222497	3434	F	1047299	5154	B	672474
1715	F	220601	3435	F	1045364	5155	B	674347
1716	F	223292	3436	F	1049803	5156	B	673238
1717	F	221403	3437	F	1047914	5157	B	675140
1718	F	223775	3438	F	1050341	5158	B	674944
1719	F	221877	3439	F	1048431	5159	B	676911
1720	F	224250	3440	F	1050862	5160	B	674797
1721	F	222377	3441	F	1048907	5161	B	676669
1722	F	224906	3442	F	1051515	5162	B	675741
1723	F	223008	3443	F	1049572	5163	B	677643
1724	F	225283	3444	F	1051828	5164	B	676340
1725	F	223418	3445	F	1049917	5165	B	678204
1726	F	226670	3446	F	1052885	5166	B	676911
1727	F	224770	3447	F	1050957	5167	B	678770
1728	F	227849	3448	F	1053963	5168	B	677240
1729	F	225937	3449	F	1052057	5169	B	679136
1730	F	228185	3450	F	1055238	5170	B	677873
1731	F	226269	3451	F	1053362	5171	B	679767
1732	F	228393	3452	F	1055849	5172	B	678549
1733	F	226512	3453	F	1053963	5173	B	680420
1734	F	229334	3454	F	1056332	5174	B	679692
1735	F	227499	3455	F	1054465	5175	B	681628
1736	F	230761	3456	F	1056738	5176	B	680320
1737	F	228846	3457	F	1054830	5177	B	682220
1738	F	231287	3458	F	1058019	5178	B	681126
1739	F	229334	3459	F	1056110	5179	B	683046
1740	F	231731	3460	F	1058504	5180	B	682558
1741	F	229927	3461	F	1056587	5181	B	684404
1742	F	232865	3462	F	1059300	5182	B	681857
1743	F	231027	3463	F	1057406	5183	B	683768
1744	F	232865	3464	F	1060356	5184	B	683046

1745	F	231027	3465	F	1058400	5185	B	684944
1746	F	234315	3466	F	1061455	5186	B	684128
1747	F	232394	3467	F	1059456	5187	B	686124
1748	F	234823	3468	F	1062092	5188	B	684893
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1750	F	235154	3470	F	1063884	5190	B	685389
1751	F	233245	3471	F	1061983	5191	B	687290
1752	F	236429	3472	F	1064928	5192	B	686207
1753	F	234520	3473	F	1063056	5193	B	688106
1754	F	237268	3474	F	1067125	5194	B	687534
1755	F	235271	3475	F	1065240	5195	B	689424
1756	F	238047	3476	F	1067963	5196	B	688416
1757	F	236162	3477	F	1066075	5197	B	690275
1758	F	238636	3478	F	1068596	5198	B	688955
1759	F	236736	3479	F	1066668	5199	B	690855
1760	F	239957	3480	F	1069752	5200	B	689727
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1762	F	241373	3482	F	1071068	5202	B	690496
1763	F	239482	3483	F	1069210	5203	B	692386
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1768	F	243281	3488	F	1075643	5208	B	695287
1769	F	241373	3489	F	1073742	5209	B	697187
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1771	F	242345	3491	F	1074450	5211	B	698172
1772	F	246052	3492	F	1077354	5212	B	696786
1773	F	244179	3493	F	1075555	5213	B	698696
1774	F	247581	3494	F	1077778	5214	B	698185
1775	F	245697	3495	F	1075880	5215	B	700090
1776	F	249216	3496	F	1078445	5216	B	700037
1777	F	247244	3497	F	1076529	5217	B	701923
1778	F	251003	3498	F	1079373	5218	B	702172
1779	F	249137	3499	F	1077523	5219	B	704050

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1784	F	253718	3504	F	1081108	5224	B	705516
1785	F	251855	3505	F	1079228	5225	B	707413
1786	F	254993	3506	F	1083006	5226	B	706312
1787	F	253138	3507	F	1081108	5227	B	708190
1788	F	256414	3508	F	1084404	5228	B	707058
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1790	F	257283	3510	F	1085896	5230	B	707856
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1794	F	258061	3514	F	1087889	5234	B	709258
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1811	F	264367	3531	F	1094509	5251	B	720383
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1813	F	265286	3533	F	1095114	5253	B	722367
1814	F	267909	3534	F	1097365	5254	B	722645

1815	F	266037	3535	F	1095498	5255	B	724559
1816	F	268594	3536	F	1097646	5256	B	723280
1817	F	266756	3537	F	1095767	5257	B	725273
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1825	F	270645	3545	F	1097547	5265	B	727988
1826	F	273007	3546	F	1100878	5266	B	727397
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1828	F	273463	3548	F	1101839	5268	B	728347
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1831	F	272057	3551	F	1102789	5271	B	730718
1832	F	275083	3552	F	1106487	5272	B	729846
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1836	F	275739	3556	F	1107814	5276	B	730377
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1842	F	277098	3562	F	1114813	5282	B	732647
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1853	F	278702	3573	F	1119202	5293	B	736978
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1856	F	282239	3576	F	1122979	5296	B	735822
1857	F	280288	3577	F	1121038	5297	B	737700
1858	F	283832	3578	F	1123376	5298	B	736099
1859	F	281933	3579	F	1121486	5299	B	737981
1860	F	284384	3580	F	1124136	5300	B	736714
1861	F	282486	3581	F	1122333	5301	B	738612
1862	F	285373	3582	F	1124623	5302	B	737448
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1864	F	285919	3584	F	1125306	5304	B	737802
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1866	F	286742	3586	F	1126300	5306	B	738048
1867	F	284879	3587	F	1124399	5307	B	739948
1868	F	287216	3588	F	1127440	5308	B	738964
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1871	F	285751	3591	F	1127134	5311	B	741190
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1873	F	286323	3593	F	1128111	5313	B	741906
1874	F	288618	3594	F	1131255	5314	B	740743
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1876	F	288273	3596	F	1132598	5316	B	741190
1877	F	286323	3597	F	1130684	5317	B	743081
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1879	F	287836	3599	F	1132002	5319	B	743875
1880	F	289508	3600	F	1134373	5320	B	743009
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1882	F	290750	3602	F	1135431	5322	B	743875
1883	F	288858	3603	F	1133531	5323	B	745738
1884	F	291142	3604	F	1135730	5324	B	744325

1885	F	289253	3605	F	1133823	5325	B	746234
1886	F	291702	3606	F	1136932	5326	B	744824
1887	F	289812	3607	F	1135040	5327	B	746724
1888	F	292522	3608	F	1139875	5328	B	745207
1889	F	290633	3609	F	1137942	5329	B	747073
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1893	F	291786	3613	F	1140366	5333	B	749206
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1898	F	296092	3618	F	1147417	5338	B	749376
1899	F	294209	3619	F	1145547	5339	B	751265
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1901	F	295757	3621	F	1146086	5341	B	752086
1902	F	298027	3622	F	1148126	5342	B	750667
1903	F	296092	3623	F	1146211	5343	B	752569
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1905	F	296582	3625	F	1147044	5345	B	753343
1906	F	299403	3626	F	1149702	5346	B	753262
1907	F	297511	3627	F	1147890	5347	B	755162
1908	F	300409	3628	F	1150561	5348	B	754535
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1910	F	301332	3630	F	1150946	5350	B	756398
1911	F	299433	3631	F	1149046	5351	B	758298
1912	F	302215	3632	F	1152302	5352	B	756708
1913	F	300282	3633	F	1150392	5353	B	758611
1914	F	302492	3634	F	1154344	5354	B	760465
1915	F	300618	3635	F	1152371	5355	B	762358
1916	F	303627	3636	F	1155448	5356	B	761441
1917	F	301730	3637	F	1153548	5357	B	763356
1918	F	304350	3638	F	1156630	5358	B	762077
1919	F	302487	3639	F	1154729	5359	B	763945

1920	F	305173	3640	F	1157756	5360	B	762528
1921	F	303226	3641	F	1155862	5361	B	764410
1922	F	306244	3642	F	1160695	5362	B	763118
1923	F	304350	3643	F	1158788	5363	B	765018
1924	F	307232	3644	F	1162326	5364	B	763539
1925	F	305310	3645	F	1160468	5365	B	765504
1926	F	307799	3646	F	1163300	5366	B	764000
1927	F	305877	3647	F	1161413	5367	B	765907
1928	F	309173	3648	F	1163763	5368	B	765391
1929	F	307301	3649	F	1161842	5369	B	767328
1930	F	310158	3650	F	1164224	5370	B	767041
1931	F	308306	3651	F	1162283	5371	B	768951
1932	F	311020	3652	F	1164800	5372	B	768271
1933	F	309118	3653	F	1162908	5373	B	770171
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1935	F	309126	3655	F	1163427	5375	B	770686
1936	F	311552	3656	F	1165877	5376	B	769562
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1938	F	312510	3658	F	1166827	5378	B	770752
1939	F	310614	3659	F	1164936	5379	B	772652
1940	F	313134	3660	F	1168099	5380	B	771701
1941	F	311255	3661	F	1166212	5381	B	773620
1942	F	313674	3662	F	1168991	5382	B	773316
1943	F	311717	3663	F	1167093	5383	B	775178
1944	F	314490	3664	F	1169769	5384	B	773690
1945	F	312633	3665	F	1167907	5385	B	775579
1946	F	315306	3666	F	1170349	5386	B	774596
1947	F	313355	3667	F	1168446	5387	B	776522
1948	F	315932	3668	F	1170953	5388	B	776300
1949	F	314033	3669	F	1169031	5389	B	778224
1950	F	318434	3670	F	1171641	5390	B	775346
1951	F	316516	3671	F	1169703	5391	B	777266
1952	F	320876	3672	F	1172172	5392	B	775618
1953	F	318949	3673	F	1170256	5393	B	777518
1954	F	321403	3674	F	1173649	5394	B	777266

1955	F	319547	3675	F	1171759	5395	B	779200
1956	F	322084	3676	F	1174885	5396	B	778224
1957	F	320217	3677	F	1172999	5397	B	780087
1958	F	322911	3678	F	1175559	5398	B	778396
1959	F	321049	3679	F	1173649	5399	B	780301
1960	F	323634	3680	F	1176927	5400	B	779557
1961	F	321726	3681	F	1175025	5401	B	781481
1962	F	325117	3682	F	1178912	5402	B	780503
1963	F	323211	3683	F	1176985	5403	B	782380
1964	F	326213	3684	F	1179826	5404	B	781419
1965	F	324254	3685	F	1177910	5405	B	783311
1966	F	327607	3686	F	1180498	5406	B	781747
1967	F	325695	3687	F	1178666	5407	B	783680
1968	F	328162	3688	F	1181716	5408	B	783004
1969	F	326262	3689	F	1179839	5409	B	784912
1970	F	328630	3690	F	1182069	5410	B	783820
1971	F	326723	3691	F	1180140	5411	B	785752
1972	F	329134	3692	F	1183626	5412	B	785255
1973	F	327178	3693	F	1181716	5413	B	787155
1974	F	330734	3694	F	1184128	5414	B	786655
1975	F	328810	3695	F	1182244	5415	B	788572
1976	F	332123	3696	F	1185004	5416	B	788671
1977	F	330252	3697	F	1183084	5417	B	790554
1978	F	334575	3698	F	1185897	5418	B	789164
1979	F	332660	3699	F	1184029	5419	B	791064
1980	F	335884	3700	F	1187151	5420	B	790001
1981	F	333980	3701	F	1185251	5421	B	791900
1982	F	337129	3702	F	1186262	5422	B	791734
1983	F	335202	3703	F	1184361	5423	B	793679
1984	F	337910	3704	F	1189054	5424	B	792944
1985	F	335955	3705	F	1187160	5425	B	794875
1986	F	338746	3706	F	1190885	5426	B	793809
1987	F	336795	3707	F	1188990	5427	B	795692
1988	F	339217	3708	F	1191507	5428	B	794580
1989	F	337362	3709	F	1189579	5429	B	796450

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1991	F	338083	3711	F	1190008	5431	B	796966
1992	F	343144	3712	F	1192524	5432	B	795956
1993	F	341266	3713	F	1190640	5433	B	797855
1994	F	343699	3714	F	1192759	5434	B	797018
1995	F	341813	3715	F	1190869	5435	B	798918
1996	F	344108	3716	F	1193642	5436	B	798989
1997	F	342204	3717	F	1191742	5437	B	800875
1998	F	344851	3718	F	1193557	5438	B	800069
1999	F	342933	3719	F	1191657	5439	B	801944
2000	F	346148	3720	F	1194015	5440	B	799840
2001	F	344219	3721	F	1192120	5441	B	801701
2002	F	346493	3722	F	1195490	5442	B	801533
2003	F	344590	3723	F	1193560	5443	B	803445
2004	F	346815	3724	F	1196093	5444	B	802717
2005	F	344907	3725	F	1194215	5445	B	804581
2006	F	347836	3726	F	1196474	5446	B	803559
2007	F	345956	3727	F	1194592	5447	B	805419
2008	F	350379	3728	F	1197659	5448	B	804032
2009	F	348432	3729	F	1195724	5449	B	805931
2010	F	350856	3730	F	1198499	5450	B	805383
2011	F	348951	3731	F	1196578	5451	B	807291
2012	F	352008	3732	F	1199912	5452	B	806107
2013	F	350106	3733	F	1197986	5453	B	807988
2014	F	353209	3734	F	1200969	5454	B	806533
2015	F	351305	3735	F	1199133	5455	B	808430
2016	F	354224	3736	F	1202121	5456	B	806954
2017	F	352312	3737	F	1200227	5457	B	808724
2018	F	354781	3738	F	1202957	5458	B	807133
2019	F	352871	3739	F	1201058	5459	B	809033
2020	F	355223	3740	F	1202590	5460	B	808442
2021	F	353261	3741	F	1200694	5461	B	810357
2022	F	355393	3742	F	1203923	5462	B	808972
2023	F	353519	3743	F	1202049	5463	B	810896
2024	F	358901	3744	F	1204631	5464	B	809674

2025	F	357001	3745	F	1202753	5465	B	811557
2026	F	356594	3746	F	1205864	5466	B	810192
2027	F	354692	3747	F	1203964	5467	B	812105
2028	F	359240	3748	F	1206483	5468	B	811472
2029	F	357374	3749	F	1204592	5469	B	813357
2030	F	359721	3750	F	1207629	5470	B	813325
2031	F	357763	3751	F	1205727	5471	B	815179
2032	F	361071	3752	F	1208802	5472	B	813133
2033	F	359240	3753	F	1206909	5473	B	815134
2034	F	363605	3754	F	1209500	5474	B	813808
2035	F	361731	3755	F	1207557	5475	B	815737
2036	F	364142	3756	F	1210483	5476	B	815246
2037	F	362246	3757	F	1208584	5477	B	817168
2038	F	364567	3758	F	1211618	5478	B	815995
2039	F	362708	3759	F	1209745	5479	B	817892
2040	F	365039	3760	F	1212523	5480	B	817264
2041	F	363184	3761	F	1210554	5481	B	819164
2042	F	365445	3762	F	1213827	5482	B	817579
2043	F	363517	3763	F	1211927	5483	B	819491
2044	F	367040	3764	F	1214875	5484	B	818890
2045	F	365144	3765	F	1212992	5485	B	820733
2046	F	368825	3766	F	1215293	5486	B	819332
2047	F	366993	3767	F	1213430	5487	B	821217
2048	F	369698	3768	F	1216043	5488	B	820096
2049	F	367760	3769	F	1214183	5489	B	821951
2050	F	370141	3770	F	1216226	5490	B	820945
2051	F	368239	3771	F	1214374	5491	B	822870
2052	F	372329	3772	F	1216927	5492	B	821151
2053	F	370375	3773	F	1215064	5493	B	823079
2054	F	372779	3774	F	1219490	5494	B	822558
2055	F	370881	3775	F	1217534	5495	B	824449
2056	F	373223	3776	F	1219431	5496	B	823767
2057	F	371342	3777	F	1217534	5497	B	825634
2058	F	373939	3778	F	1220403	5498	B	825876
2059	F	372017	3779	F	1218475	5499	B	827737

2060	F	374849	3780	F	1221383	5500	B	826583
2061	F	372953	3781	F	1219499	5501	B	828435
2062	F	375351	3782	F	1223653	5502	B	827511
2063	F	373487	3783	F	1221767	5503	B	829428
2064	F	376316	3784	F	1224758	5504	B	828829
2065	F	374416	3785	F	1222881	5505	B	830729
2066	F	377737	3786	F	1226308	5506	B	830262
2067	F	375828	3787	F	1224409	5507	B	832158
2068	F	379537	3788	F	1225625	5508	B	831286
2069	F	377660	3789	F	1223654	5509	B	833182
2070	F	380033	3790	F	1227566	5510	B	831946
2071	F	378160	3791	F	1225677	5511	B	833848
2072	F	380789	3792	F	1227858	5512	B	833372
2073	F	378889	3793	F	1225937	5513	B	835267
2074	F	381238	3794	F	1228081	5514	B	834125
2075	F	379279	3795	F	1226189	5515	B	835992
2076	F	382969	3796	B	1019	5516	B	835267
2077	F	381124	3797	B	2954	5517	B	837193
2078	F	383293	3798	B	1843	5518	B	836111
2079	F	381425	3799	B	3739	5519	B	837952
2080	F	385178	3800	B	2694	5520	B	837844
2081	F	383278	3801	B	4545	5521	B	839751
2082	F	386271	3802	B	3694	5522	B	839381
2083	F	384392	3803	B	5513	5523	B	841221
2084	F	386780	3804	B	4290	5524	B	841127
2085	F	384891	3805	B	6238	5525	B	843073
2086	F	389383	3806	B	5924	5526	B	842409
2087	F	387504	3807	B	7846	5527	B	844323
2088	F	389901	3808	B	7687	5528	B	843691
2089	F	388001	3809	B	9583	5529	B	845602
2090	F	390700	3810	B	9189	5530	B	844244
2091	F	388732	3811	B	11095	5531	B	846153
2092	F	391612	3812	B	10261	5532	B	845319
2093	F	389763	3813	B	12119	5533	B	847139
2094	F	392346	3814	B	10982	5534	B	846411

2095	F	390463	3815	B	12839	5535	B	848300
2096	F	392540	3816	B	11463	5536	B	848760
2097	F	390639	3817	B	13355	5537	B	850653
2098	F	393487	3818	B	12950	5538	B	849242
2099	F	391609	3819	B	14850	5539	B	851174
2100	F	393904	3820	B	14425	5540	B	850753
2101	F	392025	3821	B	16332	5541	B	852649
2102	F	394703	3822	B	17477	5542	B	851795
2103	F	392782	3823	B	19400	5543	B	853690
2104	F	395024	3824	B	16296	5544	B	852696
2105	F	393098	3825	B	18161	5545	B	854596
2106	F	395705	3826	B	21128	5546	B	853938
2107	F	393791	3827	B	22976	5547	B	855846
2108	F	397607	3828	B	22265	5548	B	855338
2109	F	395705	3829	B	24185	5549	B	857240
2110	F	398807	3830	B	23701	5550	B	855982
2111	F	396957	3831	B	25599	5551	B	857873
2112	F	399848	3832	B	26350	5552	B	856786
2113	F	397886	3833	B	28258	5553	B	858722
2114	F	400914	3834	B	26350	5554	B	858783
2115	F	399008	3835	B	28258	5555	B	860735
2116	F	401183	3836	B	27241	5556	B	859824
2117	F	399301	3837	B	29113	5557	B	861787
2118	F	401964	3838	B	27977	5558	B	860442
2119	F	400060	3839	B	29896	5559	B	862329
2120	F	403450	3840	B	28804	5560	B	861415
2121	F	401527	3841	B	30700	5561	B	863252
2122	F	404124	3842	B	29727	5562	B	861677
2123	F	402206	3843	B	31642	5563	B	863558
2124	F	405765	3844	B	30253	5564	B	863171
2125	F	403865	3845	B	32158	5565	B	865099
2126	F	407131	3846	B	31775	5566	B	865021
2127	F	405243	3847	B	33657	5567	B	866922
2128	F	407456	3848	B	32511	5568	B	865497
2129	F	405563	3849	B	34422	5569	B	867408

2130	F	408841	3850	B	34214	5570	B	866808
2131	F	406901	3851	B	36114	5571	B	868732
2132	F	410478	3852	B	34765	5572	B	867342
2133	F	408573	3853	B	36664	5573	B	869242
2134	F	410725	3854	B	36289	5574	B	868064
2135	F	408832	3855	B	38186	5575	B	869974
2136	F	412263	3856	B	37759	5576	B	868732
2137	F	410363	3857	B	39682	5577	B	870664
2138	F	414168	3858	B	39585	5578	B	869974
2139	F	412268	3859	B	41496	5579	B	871880
2140	F	415013	3860	B	40942	5580	B	870857
2141	F	413111	3861	B	42840	5581	B	872753
2142	F	415636	3862	B	39640	5582	B	872149
2143	F	413743	3863	B	41543	5583	B	874087
2144	F	417033	3864	B	43329	5584	B	872758
2145	F	415114	3865	B	45196	5585	B	874658
2146	F	417163	3866	B	44025	5586	B	874131
2147	F	415332	3867	B	45979	5587	B	876122
2148	F	418166	3868	B	45048	5588	B	874903
2149	F	416265	3869	B	46970	5589	B	876793
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2151	F	418259	3871	B	47472	5591	B	877437
2152	F	420697	3872	B	45979	5592	B	878078
2153	F	418861	3873	B	47901	5593	B	880011
2154	F	421313	3874	B	47216	5594	B	879478
2155	F	419437	3875	B	49128	5595	B	881385
2156	F	422172	3876	B	47791	5596	B	880874
2157	F	420342	3877	B	49689	5597	B	882771
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2159	F	421412	3879	B	50126	5599	B	884644
2160	F	424008	3880	B	49180	5600	B	883542
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2162	F	424585	3882	B	50231	5602	B	883777
2163	F	422711	3883	B	52149	5603	B	885689
2164	F	426021	3884	B	51697	5604	B	884430

2165	F	424107	3885	B	53619	5605	B	886335
2166	F	427407	3886	B	52917	5606	B	885834
2167	F	425513	3887	B	54735	5607	B	887782
2168	F	427936	3888	B	53619	5608	B	887528
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2179	F	430710	3899	B	59394	5619	B	893320
2180	F	433005	3900	B	58749	5620	B	892050
2181	F	431082	3901	B	60649	5621	B	893950
2182	F	433712	3902	B	60086	5622	B	892259
2183	F	431812	3903	B	62002	5623	B	894158
2184	F	436521	3904	B	62375	5624	B	892701
2185	F	434640	3905	B	64275	5625	B	894611
2186	F	436897	3906	B	61715	5626	B	893194
2187	F	435057	3907	B	63633	5627	B	895056
2188	F	439741	3908	B	62699	5628	B	893347
2189	F	437882	3909	B	64601	5629	B	895263
2190	F	438296	3910	B	63981	5630	B	893787
2191	F	436377	3911	B	65858	5631	B	895711
2192	F	440475	3912	B	64268	5632	B	895642
2193	F	438538	3913	B	66227	5633	B	897542
2194	F	440281	3914	B	64423	5634	B	896759
2195	F	438394	3915	B	66309	5635	B	898650
2196	F	440989	3916	B	64834	5636	B	897802
2197	F	439080	3917	B	66756	5637	B	899694
2198	F	442121	3918	B	65705	5638	B	899665
2199	F	440252	3919	B	67611	5639	B	901565

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2201	F	440221	3921	B	68163	5641	B	902360
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2203	F	440879	3923	B	69404	5643	B	905354
2204	F	443285	3924	B	67961	5644	B	905307
2205	F	441384	3925	B	69841	5645	B	907291
2206	F	444276	3926	B	68796	5646	B	907290
2207	F	442406	3927	B	70662	5647	B	909083
2208	F	444472	3928	B	70984	5648	B	908055
2209	F	442568	3929	B	72885	5649	B	909955
2210	F	444960	3930	B	69392	5650	B	908358
2211	F	443040	3931	B	71314	5651	B	910273
2212	F	445556	3932	B	71365	5652	B	908900
2213	F	443681	3933	B	73287	5653	B	910831
2214	F	447565	3934	B	72253	5654	B	909607
2215	F	445676	3935	B	74167	5655	B	911450
2216	F	448396	3936	B	73916	5656	B	911760
2217	F	446496	3937	B	75760	5657	B	913589
2218	F	450057	3938	B	76398	5658	B	912584
2219	F	448133	3939	B	78328	5659	B	914529
2220	F	450444	3940	B	77734	5660	B	913054
2221	F	448555	3941	B	79610	5661	B	914956
2222	F	450988	3942	B	78592	5662	B	914208
2223	F	449054	3943	B	80517	5663	B	916113
2224	F	452212	3944	B	79577	5664	B	915388
2225	F	450329	3945	B	81476	5665	B	917272
2226	F	453450	3946	B	79968	5666	B	915880
2227	F	451581	3947	B	81861	5667	B	917747
2228	F	454643	3948	B	80203	5668	B	916886
2229	F	452718	3949	B	82108	5669	B	918778
2230	F	456004	3950	B	80665	5670	B	917940
2231	F	454124	3951	B	82565	5671	B	919827
2232	F	456785	3952	B	81257	5672	B	919070
2233	F	454897	3953	B	83184	5673	B	920972
2234	F	457749	3954	B	83370	5674	B	920107

2235	F	455856	3955	B	85203	5675	B	922088
2236	F	458132	3956	B	84202	5676	B	920666
2237	F	456205	3957	B	86080	5677	B	922554
2238	F	459216	3958	B	85032	5678	B	921412
2239	F	457348	3959	B	86902	5679	B	923307
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2242	F	460133	3962	B	85648	5682	B	922661
2243	F	458230	3963	B	87548	5683	B	924538
2244	F	461228	3964	B	86155	5684	B	924024
2245	F	459327	3965	B	88052	5685	B	925893
2246	F	462183	3966	B	86806	5686	B	924192
2247	F	460269	3967	B	88768	5687	B	926063
2248	F	463120	3968	B	88389	5688	B	925245
2249	F	461220	3969	B	90207	5689	B	927137
2250	F	464355	3970	B	89174	5690	B	925672
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2252	F	464842	3972	B	91319	5692	B	926744
2253	F	463010	3973	B	93151	5693	B	928659
2254	F	465346	3974	B	93306	5694	B	928169
2255	F	463451	3975	B	95184	5695	B	930064
2256	F	466061	3976	B	94311	5696	B	928543
2257	F	464143	3977	B	96210	5697	B	930439
2258	F	466780	3978	B	94761	5698	B	929238
2259	F	464842	3979	B	96578	5699	B	931109
2260	F	467462	3980	B	95640	5700	B	931227
2261	F	465578	3981	B	97452	5701	B	933127
2262	F	469419	3982	B	96835	5702	B	932291
2263	F	467538	3983	B	98743	5703	B	934184
2264	F	471324	3984	B	97685	5704	B	933738
2265	F	469419	3985	B	99639	5705	B	935651
2266	F	470463	3986	B	98655	5706	B	933127
2267	F	468587	3987	B	100585	5707	B	935001
2268	F	471822	3988	B	99680	5708	B	935969
2269	F	469897	3989	B	101592	5709	B	937869

2270	F	472471	3990	B	101592	5710	B	937305
2271	F	470610	3991	B	103448	5711	B	939223
2272	F	473208	3992	B	101950	5712	B	937448
2273	F	471319	3993	B	103878	5713	B	939423
2274	F	475143	3994	B	102534	5714	B	938633
2275	F	473243	3995	B	104467	5715	B	940533
2276	F	477091	3996	B	103031	5716	B	939032
2277	F	475181	3997	B	104947	5717	B	940928
2278	F	477375	3998	B	103754	5718	B	939478
2279	F	475475	3999	B	105653	5719	B	941392
2280	F	478473	4000	B	104281	5720	B	940021
2281	F	476586	4001	B	106192	5721	B	941918
2282	F	479058	4002	B	104786	5722	B	941017
2283	F	477158	4003	B	106618	5723	B	942925
2284	F	479829	4004	B	108635	5724	B	941392
2285	F	477916	4005	B	110512	5725	B	943238
2286	F	481237	4006	B	112299	5726	B	941586
2287	F	479312	4007	B	114196	5727	B	943496
2288	F	481769	4008	B	112839	5728	B	942787
2289	F	479903	4009	B	114713	5729	B	944657
2290	F	482435	4010	B	113960	5730	B	943043
2291	F	480535	4011	B	115829	5731	B	944971
2292	F	483976	4012	B	114352	5732	B	943404
2293	F	482075	4013	B	116272	5733	B	945286
2294	F	484899	4014	B	114932	5734	B	944025
2295	F	483029	4015	B	116831	5735	B	945981
2296	F	485593	4016	B	116002	5736	B	944302
2297	F	483674	4017	B	117886	5737	B	946175
2298	F	486401	4018	B	116781	5738	B	944654
2299	F	484498	4019	B	118702	5739	B	946533
2300	F	486762	4020	B	118284	5740	B	945633
2301	F	484859	4021	B	120181	5741	B	947515
2302	F	487287	4022	B	118749	5742	B	946073
2303	F	485366	4023	B	120691	5743	B	947974
2304	F	487487	4024	B	120124	5744	B	946645

2305	F	485642	4025	B	122009	5745	B	948517
2306	F	488811	4026	B	120691	5746	B	947646
2307	F	486942	4027	B	122601	5747	B	949545
2308	F	488918	4028	B	122655	5748	B	948344
2309	F	487001	4029	B	124563	5749	B	950219
2310	F	489740	4030	B	123173	5750	B	950104
2311	F	487772	4031	B	125141	5751	B	952004
2312	F	490300	4032	B	123579	5752	B	951301
2313	F	488400	4033	B	125526	5753	B	953207
2314	F	490880	4034	B	126570	5754	B	951505
2315	F	488969	4035	B	128539	5755	B	953387
2316	F	491167	4036	B	129398	5756	B	952382
2317	F	489268	4037	B	131325	5757	B	954257
2318	F	492066	4038	B	134942	5758	B	952927
2319	F	490096	4039	B	136814	5759	B	954794
2320	F	494600	4040	B	136628	5760	B	953711
2321	F	492697	4041	B	138531	5761	B	955611
2322	F	495778	4042	B	138117	5762	B	955556
2323	F	493845	4043	B	139995	5763	B	957444
2324	F	496350	4044	B	138531	5764	B	956049
2325	F	494396	4045	B	140363	5765	B	957977
2326	F	497139	4046	B	138525	5766	B	957358
2327	F	495210	4047	B	140361	5767	B	959202
2328	F	497504	4048	B	139778	5768	B	958136
2329	F	495651	4049	B	141692	5769	B	960022
2330	F	498216	4050	B	140577	5770	B	959490
2331	F	496381	4051	B	142487	5771	B	961374
2332	F	498990	4052	B	142067	5772	B	960507
2333	F	497076	4053	B	143981	5773	B	962439
2334	F	499284	4054	B	142919	5774	B	961892
2335	F	497401	4055	B	144787	5775	B	963792
2336	F	499563	4056	B	144478	5776	B	965000
2337	F	497644	4057	B	146417	5777	B	966954
2338	F	500555	4058	B	145520	5778	B	967076
2339	F	498645	4059	B	147378	5779	B	968975

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2342	F	504574	4062	B	147545	5782	B	969039
2343	F	502741	4063	B	149452	5783	B	970930
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2346	F	507498	4066	B	148484	5786	B	970080
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2349	F	505777	4069	B	154325	5789	B	972257
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2352	F	513523	4072	B	155395	5792	B	971481
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2367	F	521123	4087	B	162572	5807	B	982862
2368	F	523865	4088	B	161075	5808	B	982167
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2387	F	532190	4107	B	171575	5827	B	990875
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2395	F	536211	4115	B	174706	5835	B	994621
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2417	F	549328	4137	B	184809	5857	B	1003941
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2420	F	554767	4140	B	185253	5860	B	1004381
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2512	F	600368	4232	B	228555	5952	B	1055816
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2517	F	600087	4237	B	231371	5957	B	1058710
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2522	F	604391	4242	B	232306	5962	B	1058919
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2547	F	614471	4267	B	244401	5987	B	1074584
2548	F	617574	4268	B	243155	5988	B	1073699
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2566	F	625263	4286	B	254230	6006	B	1081580
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2577	F	627541	4297	B	260005	6017	B	1090076
2578	F	631496	4298	B	259202	6018	B	1088704
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2580	F	633301	4300	B	261140	6020	B	1089236
2581	F	631397	4301	B	263031	6021	B	1091181
2582	F	637012	4302	B	261834	6022	B	1090076
2583	F	635112	4303	B	263716	6023	B	1091944
2584	F	638002	4304	B	263031	6024	B	1093259

2585	F	636114	4305	B	264890	6025	B	1095056
2586	F	638598	4306	B	263293	6026	B	1093403
2587	F	636682	4307	B	265179	6027	B	1095301
2588	F	638836	4308	B	264599	6028	B	1094437
2589	F	636938	4309	B	266560	6029	B	1096375
2590	F	639333	4310	B	266208	6030	B	1095839
2591	F	637471	4311	B	268109	6031	B	1097798
2592	F	640506	4312	B	266867	6032	B	1096858
2593	F	638598	4313	B	268783	6033	B	1098751
2594	F	640730	4314	B	267558	6034	B	1097305
2595	F	638885	4315	B	269472	6035	B	1099205
2596	F	641468	4316	B	268249	6036	B	1097835
2597	F	639550	4317	B	270042	6037	B	1099724
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2603	F	641229	4323	B	272920	6043	B	1100975
2604	F	643440	4324	B	271761	6044	B	1099614
2605	F	641522	4325	B	273662	6045	B	1101442
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2615	F	645712	4335	B	276716	6055	B	1108631
2616	F	648128	4336	B	275980	6056	B	1107502
2617	F	646249	4337	B	277886	6057	B	1109392
2618	F	650179	4338	B	276241	6058	B	1108337
2619	F	648244	4339	B	278138	6059	B	1110240

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2625	F	652070	4345	B	279380	6065	B	1117081
2626	F	655735	4346	B	277886	6066	B	1117154
2627	F	653827	4347	B	279722	6067	B	1119051
2628	F	656759	4348	B	278125	6068	B	1118403
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2640	F	666765	4360	B	284311	6080	B	1123752
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2644	F	668261	4364	B	285998	6084	B	1125020
2645	F	666370	4365	B	287975	6085	B	1126928
2646	F	668934	4366	B	286210	6086	B	1125790
2647	F	667029	4367	B	288110	6087	B	1127735
2648	F	670871	4368	B	287201	6088	B	1126747
2649	F	668964	4369	B	289106	6089	B	1128662
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2652	F	672231	4372	B	288217	6092	B	1128819
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2654	F	672846	4374	B	288417	6094	B	1129798

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2667	F	674888	4387	B	293372	6107	B	1138084
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2674	F	679874	4394	B	293999	6114	B	1142478
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2687	F	682410	4407	B	300899	6127	B	1151258
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2708	F	695787	4428	B	308298	6148	B	1163244
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2722	F	705018	4442	B	313687	6162	B	1168598
2723	F	703172	4443	B	315549	6163	B	1170498
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253

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2727	F	704685	4447	B	316804	6167	B	1171947
2728	F	707455	4448	B	315809	6168	B	1170689
2729	F	705553	4449	B	317701	6169	B	1172616
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2753	F	720253	4473	B	330825	6193	B	1184437
2754	F	722897	4474	B	329590	6194	B	1184078
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2756	F	723385	4476	B	331127	6196	B	1184698
2757	F	721493	4477	B	333069	6197	B	1186540
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2763	F	724143	4483	B	338267	6203	B	1188610
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2775	F	728036	4495	B	345125	6215	B	1194987
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2778	F	731760	4498	B	344391	6218	B	1194035
2779	F	729866	4499	B	346291	6219	B	1195955
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2781	F	730275	4501	B	347236	6221	B	1196265
2782	F	733018	4502	B	346289	6222	B	1194291
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2784	F	733252	4504	B	347090	6224	B	1195955
2785	F	731354	4505	B	348914	6225	B	1197863
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2787	F	731760	4507	B	349158	6227	B	1198423
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2789	F	732172	4509	B	349851	6229	B	1198951
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2791	F	732736	4511	B	352598	6231	B	1199931
2792	F	735071	4512	B	351313	6232	B	1198960
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2794	F	735381	4514	B	352400	6234	B	1200490

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2796	F	735852	4516	B	353522	6236	B	1201512
2797	F	733957	4517	B	355411	6237	B	1203426
2798	F	736244	4518	B	354690	6238	B	1202606
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2803	F	735397	4523	B	357681	6243	B	1205597
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2806	F	738491	4526	B	356173	6246	B	1205249
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2815	F	738599	4535	B	363461	6255	B	1210973
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2817	F	739676	4537	B	365905	6257	B	1211892
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2823	F	741984	4543	B	367447	6263	B	1214894
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2825	F	742365	4545	B	367873	6265	B	1216189
2826	F	744725	4546	B	366877	6266	B	1215132
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2829	F	744493	4549	B	371167	6269	B	1217542

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2831	F	745071	4551	B	371988	6271	B	1218462
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2835	F	746451	4555	B	374773	6275	B	1218973
2836	F	749395	4556	B	373315	6276	B	1219876
2837	F	747505	4557	B	375227	6277	B	1221743
2838	F	749745	4558	B	373665	6278	B	1220892
2839	F	747857	4559	B	375592	6279	B	1222895
2840	F	750165	4560	B	374428	6280	B	1220288
2841	F	748278	4561	B	376335	6281	B	1222189
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2843	F	749169	4563	B	377248	6283	B	1223517
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2849	F	754001	4569	B	379798	6289	B	1227979
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2856	F	761549	4576	B	381689	6296	B	1228524
2857	F	759660	4577	B	383629	6297	B	444
2858	F	761988	4578	B	383282	6298	B	267
2859	F	760141	4579	B	385161	6299	B	2068
2860	F	762611	4580	B	383789	6300	F	25997
2861	F	760747	4581	B	385647	6301	F	24032
2862	F	763097	4582	B	385560	6302	F	27128
2863	F	761136	4583	B	387427	6303	F	25189
2864	F	763622	4584	B	386760	6304	F	66744

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2866	F	765438	4586	B	387508	6306	F	70130
2867	F	763525	4587	B	389369	6307	F	68200
2868	F	766664	4588	B	388984	6308	F	132477
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2870	F	768045	4590	B	390387	6310	F	177854
2871	F	766196	4591	B	392260	6311	F	175906
2872	F	768329	4592	B	391202	6312	F	208127
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2874	F	769107	4594	B	392044	6314	F	208688
2875	F	767244	4595	B	393959	6315	F	206807
2876	F	770507	4596	B	392615	6316	F	208732
2877	F	768633	4597	B	394499	6317	F	206877
2878	F	771618	4598	B	393218	6318	F	210051
2879	F	769725	4599	B	395123	6319	F	208141
2880	F	772865	4600	B	393909	6320	F	298801
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2883	F	770970	4603	B	396498	6323	F	349572
2884	F	774810	4604	B	395027	6324	F	419727
2885	F	772927	4605	B	396931	6325	F	417822
2886	F	774131	4606	B	395531	6326	F	553133
2887	F	772232	4607	B	397467	6327	F	551247
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2889	F	772782	4609	B	398132	6329	F	554410
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2892	F	777314	4612	B	399189	6332	F	594641
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2894	F	777677	4614	B	400351	6334	F	661934
2895	F	775781	4615	B	402208	6335	F	660041
2896	F	778400	4616	B	401465	6336	F	706309
2897	F	776472	4617	B	403507	6337	F	704409
2898	F	779281	4618	B	401705	6338	F	803092
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2903	F	778994	4623	B	405356	6343	F	911152
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2905	F	779431	4625	B	406295	6345	F	924714
2906	F	782524	4626	B	406160	6346	F	930121
2907	F	780674	4627	B	408052	6347	F	928238
2908	F	783349	4628	B	407645	6348	F	986297
2909	F	781433	4629	B	409450	6349	F	984362
2910	F	785138	4630	B	407922	6350	F	996001
2911	F	783238	4631	B	409744	6351	F	994109
2912	F	786197	4632	B	409039	6352	F	999731
2913	F	784328	4633	B	410960	6353	F	997877
2914	F	788274	4634	B	410673	6354	F	1009782
2915	F	786387	4635	B	412559	6355	F	1007891
2916	F	788679	4636	B	411193	6356	F	1010540
2917	F	786778	4637	B	413064	6357	F	1008671
2918	F	790090	4638	B	412049	6358	F	1012465
2919	F	788213	4639	B	413946	6359	F	1010540
2920	F	791608	4640	B	414525	6360	F	1028431
2921	F	789711	4641	B	416425	6361	F	1026524
2922	F	792499	4642	B	415622	6362	F	1086215
2923	F	790605	4643	B	417559	6363	F	1084362
2924	F	793324	4644	B	416072	6364	F	1118417
2925	F	791440	4645	B	417968	6365	F	1116527
2926	F	794068	4646	B	417351	6366	F	1169595
2927	F	792185	4647	B	419259	6367	F	1167713
2928	F	794998	4648	B	417789	6368	F	1180592
2929	F	793098	4649	B	419748	6369	F	1178709
2930	F	795457	4650	B	418569	6370	F	1182406
2931	F	793582	4651	B	420453	6371	F	1180498
2932	F	796831	4652	B	420345	6372	F	1194573
2933	F	794931	4653	B	422177	6373	F	1192667
2934	F	798455	4654	B	421003	6374	F	1195654

2935	F	796551	4655	B	422873	6375	F	1193753
2936	F	799056	4656	B	421819	6376	B	26870
2937	F	797147	4657	B	423675	6377	B	28721
2938	F	799558	4658	B	422291	6378	B	27835
2939	F	797649	4659	B	424158	6379	B	29730
2940	F	801106	4660	B	423186	6380	B	67456
2941	F	799204	4661	B	425075	6381	B	69351
2942	F	802227	4662	B	424544	6382	B	70820
2943	F	800325	4663	B	426443	6383	B	72708
2944	F	803050	4664	B	424859	6384	B	133173
2945	F	801153	4665	B	426714	6385	B	135068
2946	F	803599	4666	B	426302	6386	B	178637
2947	F	801682	4667	B	428193	6387	B	180518
2948	F	804925	4668	B	427640	6388	B	208864
2949	F	803016	4669	B	429523	6389	B	210727
2950	F	805633	4670	B	428212	6390	B	209376
2951	F	803672	4671	B	430111	6391	B	211305
2952	F	806109	4672	B	428709	6392	B	209483
2953	F	804192	4673	B	430627	6393	B	211383
2954	F	806386	4674	B	430926	6394	B	210875
2955	F	804453	4675	B	432851	6395	B	212766
2956	F	806668	4676	B	431681	6396	B	299694
2957	F	804746	4677	B	433569	6397	B	301582
2958	F	807924	4678	B	432324	6398	B	352312
2959	F	806022	4679	B	434223	6399	B	354200
2960	F	808445	4680	B	433015	6400	B	420390
2961	F	806525	4681	B	434902	6401	B	422291
2962	F	809212	4682	B	433504	6402	B	553822
2963	F	807283	4683	B	435426	6403	B	555736
2964	F	809982	4684	B	434196	6404	B	557050
2965	F	808079	4685	B	436042	6405	B	558930
2966	F	811554	4686	B	436913	6406	B	594583
2967	F	809659	4687	B	438807	6407	B	596527
2968	F	812268	4688	B	437475	6408	B	595405
2969	F	810340	4689	B	439423	6409	B	597289

2970	F	812712	4690	B	438591	6410	B	662614
2971	F	810799	4691	B	440490	6411	B	664530
2972	F	813355	4692	B	440583	6412	B	707138
2973	F	811466	4693	B	442491	6413	B	709063
2974	F	815198	4694	B	440583	6414	B	803951
2975	F	813243	4695	B	442441	6415	B	805790
2976	F	815798	4696	B	441274	6416	B	849771
2977	F	813917	4697	B	443135	6417	B	851730
2978	F	816879	4698	B	441459	6418	B	913917
2979	F	814940	4699	B	443353	6419	B	915796
2980	F	817571	4700	B	442412	6420	B	927331
2981	F	815676	4701	B	444339	6421	B	929238
2982	F	818388	4702	B	443184	6422	B	930857
2983	F	816489	4703	B	445100	6423	B	932735
2984	F	818884	4704	B	443131	6424	B	986987
2985	F	816921	4705	B	445100	6425	B	988912
2986	F	819597	4706	B	443800	6426	B	996771
2987	F	817680	4707	B	445789	6427	B	998623
2988	F	820485	4708	B	444771	6428	B	1000593
2989	F	818555	4709	B	446620	6429	B	1002496
2990	F	820764	4710	B	445100	6430	B	1010541
2991	F	818878	4711	B	446962	6431	B	1012452
2992	F	821982	4712	B	445229	6432	B	1011365
2993	F	820080	4713	B	447187	6433	B	1013249
2994	F	823403	4714	B	445974	6434	B	1013146
2995	F	821559	4715	B	447872	6435	B	1015044
2996	F	825235	4716	B	448028	6436	B	1029168
2997	F	823320	4717	B	449927	6437	B	1031036
2998	F	826405	4718	B	448958	6438	B	1087041
2999	F	824501	4719	B	450858	6439	B	1088885
3000	F	826945	4720	B	449850	6440	B	1119102
3001	F	825046	4721	B	451753	6441	B	1121033
3002	F	828489	4722	B	451103	6442	B	1170355
3003	F	826588	4723	B	453045	6443	B	1172218
3004	F	829813	4724	B	451482	6444	B	1181427

3005	F	827917	4725	B	453330	6445	B	1183338
3006	F	830824	4726	B	452676	6446	B	1183263
3007	F	828906	4727	B	454575	6447	B	1185158
3008	F	831936	4728	B	453884	6448	B	1195296
3009	F	830099	4729	B	455783	6449	B	1197175
3010	F	833126	4730	B	455068	6450	B	1196406
3011	F	831274	4731	B	456963	6451	B	1198306

TABLE 6

clone Name	SEQ ID NO (B)	SEQ ID NO (F)	Chromosomal region
790313H3#	6452	6648	A
790331B1#	6453	6649	A
790233A9#	6454	6650	A
790031G7#	6455	6651	A
890021E4#	6456	6652	A
790021E11#	6457	6653	A
790332G10#	6458	6654	A
790271B6#	6459	6655	A
790253H6#	6460	6656	A
790214E8#	6461	6657	A
790352D2#	6462	6658	A
790373F2#	6463	6659	A
790424A7#	6464	6660	A
790282F3#	6465	6661	A
790272F5#	6466	6662	A
790424F6#	6467	6663	A
890033H11#	6468	6664	A
790264H10#	6469	6665	A
790293A5#	6470	6666	A
790391E8#	6471	6667	A
890022B8#	6472	6668	A
790332B9#	6473	6669	A
790251B9#	6474	6670	A
790344E8#	6475	6671	B
790323F3#	6476	6672	B
790231G2#	6477	6673	B
790341C5#	6478	6674	B
790332H9#	6479	6675	B
890013A8#	6480	6676	B
790394F2#	6481	6677	B
790222G5#	6482	6678	B
790402A10#	6483	6679	B
790283F6#	6484	6680	B

790041H11#	6485	6681	B
790381C7#	6486	6682	B
790213E1#	6487	6683	B
790211C4#	6488	6684	B
790251B5#	6489	6685	B
790043H9#	6490	6686	B
790303F7#	6491	6687	B
790251G5#	6492	6688	B
790044H7#	6493	6689	B
790022E4#	6494	6690	B
790252A8#	6495	6691	B
790313E9#	6496	6692	B
790264G2#	6497	6693	B
790372A4#	6498	6694	B
790411C2#	6499	6695	B
790322B7#	6500	6696	B
790254F7#	6501	6697	B
790323B12#	6502	6698	B
790263E5#	6503	6699	B
790223C8#	6504	6700	B
790231H2#	6505	6701	B
790324E12#	6506	6702	B
790271D7#	6507	6703	B
790222E8#	6508	6704	B
790083G7#	6509	6705	B
790241D3#	6510	6706	B
790303C8#	6511	6707	B
790283F10#	6512	6708	B
790241B7#	6513	6709	B
790373F10#	6514	6710	B
790362F9#	6515	6711	B
790263H8#	6516	6712	B
790393D10#	6517	6713	B
790313D12#	6518	6714	B
890024C6#	6519	6715	B

890024B10#	6520	6716	B
790212E2#	6521	6717	B
790362E10#	6522	6718	B
790344G11#	6523	6719	B
890011D2#	6524	6720	B
790341B11#	6525	6721	B
790064E10#	6526	6722	B
790212E1#	6527	6723	B
790213G5#	6528	6724	B
790331F2#	6529	6725	B
890024B9#	6530	6726	B
790421F5#	6531	6727	B
890014D11#	6532	6728	B
790373F3#	6533	6729	B
790293D4#	6534	6730	B
790211A3#	6535	6731	B
790211H8#	6536	6732	B
790264E7#	6537	6733	B
790292B11#	6538	6734	B
790312A2#	6539	6735	B
890012D5#	6540	6736	B
790012D12#	6541	6737	B
790291E10#	6542	6738	B
790241C9#	6543	6739	B
790343F1#	6544	6740	B
790241D7#	6545	6741	B
790031H7#	6546	6742	B
790081C4#	6547	6743	B
790013B7#	6548	6744	B
790213F3#	6549	6745	B
790292F9#	6550	6746	B
790423F4#	6551	6747	B
790331F3#	6552	6748	B
790222B10#	6553	6749	B
790261G12#	6554	6750	B

790423G10#	6555	6751	B
790392A9#	6556	6752	B
790331B5#	6557	6753	B
790323H3#	6558	6754	B
890014H8#	6559	6755	B
790231B6#	6560	6756	B
790252F7#	6561	6757	B
790392C10#	6562	6758	B
790021D4#	6563	6759	B
790052D10#	6564	6760	B
790261E3#	6565	6761	B
890023E10#	6566	6762	B
790244B7#	6567	6763	B
790383E1#	6568	6764	B
790401B11#	6569	6765	B
790411B5#	6570	6766	B
790423A11#	6571	6767	B
790031A4#	6572	6768	B
790241G3#	6573	6769	B
790044F7#	6574	6770	B
790252B10#	6575	6771	B
790293F9#	6576	6772	B
790282H3#	6577	6773	B
790381C10#	6578	6774	B
790024H5#	6579	6775	B
790354H7#	6580	6776	B
790411F9#	6581	6777	B
790324G10#	6582	6778	B
790014A5#	6583	6779	B
790381F3#	6584	6780	B
790424D3#	6585	6781	B
790394A10#	6586	6782	B
790423C10#	6587	6783	B
790214D6#	6588	6784	B
790214C4#	6589	6785	B

790014F11#	6590	6786	B
790352F10#	6591	6787	B
790381H6#	6592	6788	B
790282G5#	6593	6789	B
790263C8#	6594	6790	B
890022B4#	6595	6791	B
790283C6#	6596	6792	B
790293B2#	6597	6793	B
790073A3#	6598	6794	B
790313E10#	6599	6795	B
790361D3#	6600	6796	B
790014A11#	6601	6797	B
790254G2#	6602	6798	B
790381C6#	6603	6799	B
790424E3#	6604	6800	B
790421G8#	6605	6801	B
790013C3#	6606	6802	B
790263E8#	6607	6803	B
790373C1#	6608	6804	B
790041C1#	6609	6805	B
790344A7#	6610	6806	B
790271D6#	6611	6807	B
790342H2#	6612	6808	B
890021A6#	6613	6809	B
790381E7#	6614	6810	C
790013G10#	6615	6811	C
790254A4#	6616	6812	C
790213D8#	6617	6813	C
790052A4#	6618	6814	C
790213D3#	6619	6815	C
790394D2#	6620	6816	C
790214D2#	6621	6817	C
790014A4#	6622	6818	C
790324H4#	6623	6819	C
790082B4#	6624	6820	C

790324A6#	6625	6821	C
790424A12#	6626	6822	C
790044G8#	6627	6823	C
790323C6#	6628	6824	C
790312G4#	6629	6825	C
790053C11#	6630	6826	C
890022B7#	6631	6827	C
790392A2#	6632	6828	C
890023D8#	6633	6829	C
790301F1#	6634	6830	C
790343A11#	6635	6831	C
790421A2#	6636	6832	C
790271G2#	6637	6833	C
790302G12#	6638	6834	C
790341E5#	6639	6835	C
790283B6#	6640	6836	C
790222A4#	6641	6837	C
790241B8#	6642	6838	C
790014C2#	6643	6839	C
790402C1#	6644	6840	C
790264E9#	6645	6841	C
790242G4#	6646	6842	C
790422F3#	6647	6843	C

TABLE 7

SEQ ID	or.	5'position	SEQ ID	or.	5'position	SEQ ID	or.	5'position
6452	B	29372	6583	B	547718	6714	F	519646
6453	B	30198	6584	B	547184	6715	F	520201
6454	B	31007	6585	B	547684	6716	F	520563
6455	B	31126	6586	B	547342	6717	F	521015
6456	B	32735	6587	B	548946	6718	F	521162
6457	B	32264	6588	B	549071	6719	F	521543
6458	B	32898	6589	B	550054	6720	F	521739
6459	B	33582	6590	B	549989	6721	F	522328
6460	B	33519	6591	B	550426	6722	F	522567
6461	B	34836	6592	B	550055	6723	F	522915
6462	B	35795	6593	B	550132	6724	F	523300
6463	B	35548	6594	B	550132	6725	F	523791
6464	B	35825	6595	B	551400	6726	F	523959
6465	B	37239	6596	B	551572	6727	F	524369
6466	B	36761	6597	B	551468	6728	F	524801
6467	B	37045	6598	B	550849	6729	F	525085
6468	B	36761	6599	B	552137	6730	F	525241
6469	B	37958	6600	B	552325	6731	F	525738
6470	B	38636	6601	B	552583	6732	F	526263
6471	B	39813	6602	B	553033	6733	F	526628
6472	B	41140	6603	B	553629	6734	F	526779
6473	B	40575	6604	B	553960	6735	F	527004
6474	B	40526	6605	B	553914	6736	F	527230
6475	B	501495	6606	B	554354	6737	F	527381
6476	B	502410	6607	B	555783	6738	F	527545
6477	B	502586	6608	B	555687	6739	F	527691
6478	B	503233	6609	B	556441	6740	F	527932
6479	B	503749	6610	B	557054	6741	F	527995
6480	B	504488	6611	B	556627	6742	F	528167
6481	B	504206	6612	B	557292	6743	F	528610
6482	B	504310	6613	B	557050	6744	F	529063
6483	B	505455	6614	B	815995	6745	F	529710
6484	B	505877	6615	B	817104	6746	F	531140

6485	B	506655	6616	B	817104	6747	F	531488
6486	B	506513	6617	B	816920	6748	F	531842
6487	B	507532	6618	B	820464	6749	F	532064
6488	B	507742	6619	B	821017	6750	F	532350
6489	B	508050	6620	B	821379	6751	F	532794
6490	B	507771	6621	B	821504	6752	F	533117
6491	B	509120	6622	B	822723	6753	F	533536
6492	B	509646	6623	B	823298	6754	F	533868
6493	B	510137	6624	B	823380	6755	F	534200
6494	B	510953	6625	B	824414	6756	F	534844
6495	B	511165	6626	B	824204	6757	F	535213
6496	B	511526	6627	B	825288	6758	F	535678
6497	B	511993	6628	B	825346	6759	F	535970
6498	B	513012	6629	B	825403	6760	F	536504
6499	B	512983	6630	B	826237	6761	F	537013
6500	B	512781	6631	B	824995	6762	F	537710
6501	B	514155	6632	B	826838	6763	F	538047
6502	B	515036	6633	B	828146	6764	F	538353
6503	B	515287	6634	B	827878	6765	F	538718
6504	B	516292	6635	B	827571	6766	F	539188
6505	B	516234	6636	B	828472	6767	F	539471
6506	B	516337	6637	B	828484	6768	F	539910
6507	B	517347	6638	B	828691	6769	F	540774
6508	B	517005	6639	B	829507	6770	F	540962
6509	B	516888	6640	B	829169	6771	F	541721
6510	B	516234	6641	B	828763	6772	F	542198
6511	B	517560	6642	B	829769	6773	F	542644
6512	B	517337	6643	B	831582	6774	F	543180
6513	B	518756	6644	B	830481	6775	F	543877
6514	B	518943	6645	B	831468	6776	F	544601
6515	B	519833	6646	B	831670	6777	F	544866
6516	B	520123	6647	B	832293	6778	F	545442
6517	B	520574	6648	F	28484	6779	F	545948
6518	B	520888	6649	F	29043	6780	F	546209
6519	B	522154	6650	F	29656	6781	F	546585

6520	B	523041	6651	F	30157	6782	F	546960
6521	B	522052	6652	F	30712	6783	F	547114
6522	B	522217	6653	F	31175	6784	F	547726
6523	B	523035	6654	F	31658	6785	F	548045
6524	B	524995	6655	F	31902	6786	F	548480
6525	B	523567	6656	F	32638	6787	F	548561
6526	B	523477	6657	F	33203	6788	F	548775
6527	B	523967	6658	F	33804	6789	F	549037
6528	B	525211	6659	F	34164	6790	F	549153
6529	B	525215	6660	F	34426	6791	F	549597
6530	B	526133	6661	F	35131	6792	F	550049
6531	B	525674	6662	F	35675	6793	F	550520
6532	B	526561	6663	F	36097	6794	F	550890
6533	B	526697	6664	F	36641	6795	F	550997
6534	B	526715	6665	F	36835	6796	F	551040
6535	B	526844	6666	F	37236	6797	F	551247
6536	B	527261	6667	F	38287	6798	F	551854
6537	B	527503	6668	F	38711	6799	F	552333
6538	B	528775	6669	F	39117	6800	F	552603
6539	B	528249	6670	F	39798	6801	F	552823
6540	B	530307	6671	F	500539	6802	F	553207
6541	B	527772	6672	F	501016	6803	F	553898
6542	B	529406	6673	F	501319	6804	F	554298
6543	B	527752	6674	F	501632	6805	F	554767
6544	B	529829	6675	F	502155	6806	F	555323
6545	B	529907	6676	F	502623	6807	F	555595
6546	B	529574	6677	F	503025	6808	F	555965
6547	B	529635	6678	F	503681	6809	F	556248
6548	B	530391	6679	F	504389	6810	F	815116
6549	B	531516	6680	F	504744	6811	F	815376
6550	B	532154	6681	F	505468	6812	F	815849
6551	B	532606	6682	F	505652	6813	F	816098
6552	B	533407	6683	F	505822	6814	F	818726
6553	B	533664	6684	F	505833	6815	F	819337
6554	B	533916	6685	F	506933	6816	F	820080

6555	B	534707	6686	F	507220	6817	F	820750
6556	B	533482	6687	F	507559	6818	F	821170
6557	B	534614	6688	F	508216	6819	F	821815
6558	B	534935	6689	F	508619	6820	F	822490
6559	B	536823	6690	F	509329	6821	F	822789
6560	B	535986	6691	F	509783	6822	F	823244
6561	B	536143	6692	F	510383	6823	F	823762
6562	B	537505	6693	F	510729	6824	F	823964
6563	B	537618	6694	F	511188	6825	F	824245
6564	B	538165	6695	F	511773	6826	F	824609
6565	B	538702	6696	F	511869	6827	F	824948
6566	B	540278	6697	F	512946	6828	F	825490
6567	B	539156	6698	F	513202	6829	F	826064
6568	B	539619	6699	F	513821	6830	F	826405
6569	B	540115	6700	F	514322	6831	F	826480
6570	B	540724	6701	F	514811	6832	F	827089
6571	B	541484	6702	F	515101	6833	F	827418
6572	B	540968	6703	F	515611	6834	F	827496
6573	B	542062	6704	F	515911	6835	F	827730
6574	B	541898	6705	F	516123	6836	F	828180
6575	B	543100	6706	F	516169	6837	F	828348
6576	B	543846	6707	F	516215	6838	F	828729
6577	B	543820	6708	F	516305	6839	F	830099
6578	B	544382	6709	F	517240	6840	F	830281
6579	B	545158	6710	F	517993	6841	F	830491
6580	B	545678	6711	F	518174	6842	F	830550
6581	B	545905	6712	F	518756	6843	F	830576
6582	B	546683	6713	F	519133			

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WHAT IS CLAIMED IS:

1- An isolated polynucleotide having a nucleotide sequence of a *Chlamydia pneumoniae* genome, comprising

    (a)   the a nucleotide sequence of SEQ ID No. 1;

    (b)   the nucleotide sequence contained within the *Chlamydia pneumoniae* genomic DNA in ATCC Deposit No. _____;

    (c)   the nucleotide sequence contained in a clone insert in ATCC Deposit No. _____;

    (d)   a nucleotide sequence exhibiting at least 99.9% identity with the sequence of SEQ ID No. 1; or

    (e)   a nucleotide sequence exhibiting at least 80% homology to SEQ ID No. 1.

2- An isolated polynucleotide which hybridizes to SEQ ID No. 1 or to the *Chlamydia pneumoniae* genomic DNA contained in ATCC deposit No. _____ or to a clone insert in ATCC Deposit No. _____ under conditions of high stringency.

3- An isolated polynucleotide which hybridizes to SEQ ID No. 1 or to the *Chlamydia pneumoniae* genomic DNA contained in ATCC deposit No. _____ under conditions of intermediate stringency.

4- An isolated polynucleotide having a nucleotide sequence of an open reading frame (ORF) of a *Chlamydia pneumoniae* genome, comprising:

    (a)   a nucleotide sequence chosen from one of ORF2 to ORF 1297;

    (b)   a nucleotide sequence exhibiting at least 99.9% identity with one of ORF2 to ORF 1297; or

    (c)   a nucleotide sequence exhibiting at least 80% homology to one of ORF2 to ORF 1297.

5- An isolated polynucleotide which hybridizes to one of ORF2 to ORF 1297 under conditions of high stringency.

6- An isolated polynucleotide which hybridizes to one of ORF2 to ORF 1297 under conditions of intermediate stringency.

7- The polynucleotide of Claims 2, 3, 4, 5, or 6 which encodes the following polypeptides or fragments thereof:

    (a)   a *Chlamydia pneumoniae* transmembrane polypeptide having between 1 and 3 transmembrane domains;

(b)   a *Chlamydia pneumoniae* transmembrane polypeptide having between 4 and 6 transmembrane domains;

(c)   a *Chlamydia pneumoniae* transmembrane polypeptide having at least 7 transmembrane domains;

(d)   a *Chlamydia pneumoniae* polypeptide involved in intermediate metabolism of sugars and/or cofactors;

(e)   a *Chlamydia pneumoniae* polypeptide involved in intermediate metabolism of nucleotides or nucleic acids;

(f)   a *Chlamydia pneumoniae* polypeptide involved in metabolism of amino acids or polypeptides;

(g)   a *Chlamydia pneumoniae* polypeptide having involved in metabolism of fatty acids;

(h)   a *Chlamydia pneumoniae* polypeptide involved in the synthesis of the cell wall;

(i)   a *Chlamydia pneumoniae* polypeptide involved in transcription, translation, and/or maturation process;

(j)   a *Chlamydia pneumoniae* transport polypeptide;

(k)   a *Chlamydia pneumoniae* polypeptide involved in the virulence process;

(l)   a *Chlamydia pneumoniae* polypeptide involved in the secretory system and/or which is secreted;

(m)   a *Chlamydia pneumoniae* polypeptide of the cellular envelope or outer cellular envelope of *Chlamydia pneumoniae*.

(n)   a *Chlamydia pneumoniae* surface exposed polypeptide;

(o)   a *Chlamydia pneumoniae* lipoprotein;

(p)   a *Chlamydia pneumoniae* polypeptide involved in lipopolysaccharide biosynthesis;

(q)   a *Chlamydia pneumoniae* KDO-related polypeptide;

(r)   a *Chlamydia pneumoniae* phosphomannomutase-related polypeptide;

(s)   a *Chlamydia pneumoniae* lipid A component-related polypeptide;

(t)   a *Chlamydia pneumoniae* phosphoglucomutase-related polypeptide;

(u)   a *Chlamydia pneumoniae* polypeptide that contains an RGD sequence;

(v)   a *Chlamydia pneumoniae* Type III secreted polypeptide;

(w)   a *Chlamydia pneumoniae* cell wall anchored surface polypeptide; or

(x)   a *Chlamydia pneumoniae* polypeptide that is not found in *Chlamydia trachomatis*.

8- A polynucleotide encoding a fusion protein, comprising one of ORF2 to ORF1297 of Claim 4, 5, or 6 ligated in frame to a polynucleotide encoding a heterologous polypeptide.

9- A recombinant vector that contains the polynucleotide of Claim 1, 2, 3, 4, 5 or 6.

10- A recombinant vector that contains the polynucleotide of Claim 8.

11- A recombinant vector that contains the polynucleotide of Claim 4, 5 or 6, operatively associated with a regulatory sequence that controls gene expression.

12- A recombinant vector that contains the polynucleotide of Claim 8 operatively associated with a regulatory sequence that controls gene expression.

13- A genetically engineered host cell that contains the polynucleotide of Claim 1, 2, 3, 4, 5 or 6.

14- A genetically engineered host cell that contains the polynucleotide of Claim 8.

15- A genetically engineered host cell that contains the polynucleotide of Claim 4, 5 or 6 operatively associated with a regulatory sequence that controls gene expression in the host cell.

16- A genetically engineered host cell that contains the polynucleotide of Claim 8 operatively associated with a regulatory sequence that controls gene expression in the host cell.

17- A method for producing a polypeptide, comprising:

       (a)   culturing the genetically engineered host cell of Claim 15 under conditions suitable to produce the polypeptide encoded by the polynucleotide; and

       (b)   recovering the polypeptide from the culture.

18- A method for producing a fusion protein, comprising:

       (a)   culturing the genetically engineered host cell of Claim 16 under conditions suitable to produce the fusion protein encoded by the polynucleotide; and

       (b)   recovering the fusion protein from the culture.

19- A polypeptide encoded by the polynucleotide of Claim 4, 5 or 6.

20- The polypeptide of Claim 19 which immunoreacts with seropositive serum of an
individual infected with *Chlamydia pneumoniae.*

21- The polypeptide of Claim 19 which comprises the following polypeptides or fragments
thereof:

(a)   a *Chlamydia pneumoniae* transmembrane polypeptide having
      between 1 and 3 transmembrane domains;

(b)   a *Chlamydia pneumoniae* transmembrane polypeptide having
      between 4 and 6 transmembrane domains;

(c)   a *Chlamydia pneumoniae* transmembrane polypeptide having at
      least 7 transmembrane domains;

(d)   a *Chlamydia pneumoniae* polypeptide involved in intermediate
      metabolism of sugars and/or cofactors;

(e)   a *Chlamydia pneumoniae* polypeptide involved in intermediate
      metabolism of nucleotides or nucleic acids;

(f)   a *Chlamydia pneumoniae* polypeptide involved in metabolism
      of amino acids or polypeptides;

(g)   a *Chlamydia pneumoniae* polypeptide involved in metabolism
      of fatty acids;

(h)   a *Chlamydia pneumoniae* polypeptide involved in the synthesis
      of the cell wall;

(i)   a *Chlamydia pneumoniae* polypeptide involved in transcription,
      translation, and/or maturation process;

(j)   a *Chlamydia pneumoniae* transport polypeptide;

(k)   a *Chlamydia pneumoniae* polypeptide involved in the virulence
      process;

(l)   a *Chlamydia pneumoniae* polypeptide involved in the secretory
      system and/or which is secreted;

(m)   a *Chlamydia pneumoniae* polypeptide of the cellular envelope
      or outer cellular envelope of *Chlamydia pneumoniae.*

(n)   a *Chlamydia pneumoniae* surface exposed polypeptide;

(o)   a *Chlamydia pneumoniae* lipoprotein;

(p)   a *Chlamydia pneumoniae* polypeptide involved in
      lipopolysaccharide biosynthesis;

(q)   a *Chlamydia pneumoniae* KDO-related polypeptide;

282

    (r)   a   *Chlamydia*   *pneumoniae*   phosphomannomutase-related polypeptide;

    (s)   a   *Chlamydia*   *pneumoniae*   phosphoglucomutase-related polypeptide;

    (t)   a   *Chlamydia*   *pneumoniae*   lipid   A   component-related polypeptide;

    (u)   a *Chlamydia pneumoniae* polypeptide that contains an RGD sequence;

    (v)   a *Chlamydia pneumoniae* Type III secreted polypeptide;

    (w)   a   *Chlamydia*   *pneumoniae*   cell   wall   anchored   surface polypeptide; or

    (x)   a *Chlamydia pneumoniae* polypeptide that is not found in *Chlamydia trachomatis*.

22- A fusion protein encoded by the polynucleotide of Claim 8.

23- The fusion protein of Claim 22 which immunoreacts with seropositive serum of an individual infected with *Chlamydia pneumoniae*.

24- An antibody that immunospecifically binds to the polypeptide of Claim 19.

25- An antibody that immunospecifically binds to the fusion protein of Claim 22.

26- A method for the detection and/or identification of *Chlamydia pneumoniae* in a biological sample, comprising:

    (a)   contacting the sample with a polynucleotide primer of Claim 1, 2, 3, 4, 5, or 6 in the presence of a polymerase enzyme and nucleotides under conditions which permit primer extension; and

    (b)   detecting the presence of primer extension products in the sample in which the detection of primer extension products indicates the presence of *Chlamydia pneumoniae* in the sample.

27- A method for the detection and/or identification of *Chlamydia pneumoniae* in a biological sample, comprising:

    (a)   contacting the sample with a polynucleotide probe of Claim 1, 2, 3, 4, 5, or 6 under conditions which permit hybridization of complementary base pairs; and

(b)   detecting the presence of hybridization complexes in the sample
in which the detection of hybridization complexes indicates the
presence of *Chlamydia pneumoniae* in the sample.

28- A method for the detection and/or identification of *Chlamydia pneumoniae* in a biological
sample, comprising:

(a)   contacting the sample with the antibody of Claim 24 under
conditions suitable for the formation of immune complexes; and

(b)   detecting the presence of immune complexes in the sample, in
which the detection of immune complexes indicates the
presence of *Chlamydia pneumoniae* in the sample.

29- A method for the detection and/or identification of antibodies to *Chlamydia pneumoniae*
in a biological sample, comprising:

(a)   contacting the sample with a polypeptide of Claim 19 under
conditions suitable for the formation of immune complexes; and

(b)   detecting the presence of immune complexes in the sample, in
which the detection of immune complexes indicates the
presence of *Chlamydia pneumoniae* in the sample.

30- A DNA chip containing an array of polynucleotides comprising at least one of the
polynucleotides of Claim 1, 2, 3, 4, 5, or 6.

31- A protein chip containing an array of polypeptides comprising at least one of the
polypeptides of Claim 19.

32- An immunogenic composition comprising the polypeptide of Claim 19 and a
pharmaceutically acceptable carrier.

33- An immunogeneic composition comprising the polypeptide of Claim 20 and a
pharmaceutically acceptable carrier.

34- An immunogenic composition comprising the fusion protein of Claim 22 and a
pharmaceutically acceptable carrier.

35- An immunogenic composition comprising the fusion protein of Claim 23 and a
pharmaceutically acceptable carrier.

36- A pharmaceutical composition comprising the polypeptide of Claim 19 and a pharmaceutically acceptable carrier.

37- A pharmaceutical composition comprising the polypeptide of Claim 20 and a pharmaceutically acceptable carrier.

38- A pharmaceutical composition comprising the polypeptide of Claim 22 and a pharmaceutically acceptable carrier.

39- A pharmaceutical composition comprising the polypeptide of Claim 23 and a pharmaceutically acceptable carrier.

40- A method of immunizing against *Chlamydia pneumoniae*, comprising: administering to a host an immunizing amount of the immunogenic composition of Claim 32.

41- A method of immunizing against *Chlamydia pneumoniae*, comprising: administering to a host an immunizing amount of the immunogenic composition of Claim 33.

42- A method of immunizing against *Chlamydia pneumoniae*, comprising administering to a host an immunizing amount of the immunogenic composition of Claim 34.

43- A method of immunizing against *Chlamydia pneumoniae*, comprising: administering to a host an immunizing amount of the immunogenic composition of Claim 35.

44- A DNA immunogenic composition comprising the expression vector of Claim 11.

45- The DNA composition of Claim 44, wherein the DNA composition directs the expression of a neutralizing epitope of *Chlamydia pneumoniae*.

46- A DNA immunogenic composition comprising the expression vector of Claim 12.

47- The DNA composition of Claim 46, wherein the DNA composition directs the expression of a neutralizing epitope of *Chlamydia pneumoniae*.

48- A screening assay, comprising:

    (a)   contacting a test compound with an isolated polynucleotide of Claim 1, 2, 3, 4, 5 or 6; and

    (b)   detecting whether binding occurs.

49- A screening assay, comprising:

    (a)   contacting a test compound with the polypeptide of Claim19; and

    (b)   detecting whether binding occurs.

50- A screening assay, comprising:

    (a)   contacting a test compound with the polypeptide of Claim 22; and

    (b)   detecting whether binding occurs.

51- A kit comprising a container containing an isolated polynucleotide of Claim 1, 2, 3, 4, 5 or 6.

52- The kit of Claim 51 wherein the polynucleotide is a primer or a probe.

53- The kit of Claim 51 wherein the polynucleotide is a primer and the kit further comprises a container containing a polymerase.

54- The kit of Claim 51 which further comprises a container containing deoxynucleotide triphosphates.

55- A kit comprising a container containing an antibody that immunospecifically binds to the polypeptide of Claim 19.

56- A kit comprising a container containing an antibody that immunospecifically binds to the fusion protein of Claim 22.

Figure 1.

Figure 2.

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...
>91006-1D6.B
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GAGATTATTACGACAG...
...
>....

STADEN Package
Sun Solaris

TIGR Asmg
Sun Solaris

Comparison of
the results

PC/Windows NT:

Manufacture of assembly map:

●Relationship and orientation of
the "contigs" in relation to each
other.

●Determination of the clones useful
for obtaining the missing sequences
between the "contigs"

●Choice of the PCR and sequencing
primers for obtaining the missing
sequences between the "contigs"

Figure 3a

●Determination of the ends of the
"contigs" having no relationship
with other "contigs" (orphan ends)

●Choice of the PCR primers which
make it possible to study the
relationship between the orphan ends

Figure 3b

FIGURE 3A

Contig A

S1

Contig B

S2

Distribution and position of the sequences on the contigs:

1- Define the arrangement of the contigs in relation to each other

2- Define the PCR primers which make it possible to fill the sequence

Contig A

S1

Contig B

S2

Statistical determination of the sequences:

1- Belonging to the same clone

2- Situated on two different contigs

FIGURE 3B

Contig A

S1

Contig B

S2

Cp18   E   I   E

Cp1   E   I   E

Contig D

S5

Contig C

S4

Contig ends without connecting clone:

1- Identification of the ends

2- Determination of outer and inner PCR primers for studying the relationships between the contigs

E: outer primers

I: inner primers

SEQUENCE LISTING

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thereof and uses thereof, in particular for the diagnosis, prevention
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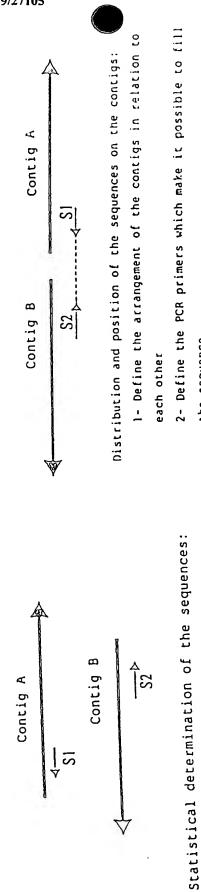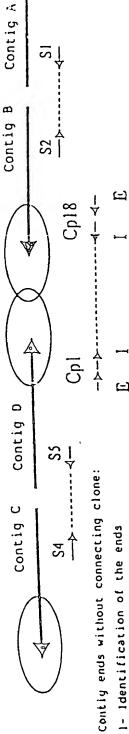
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23

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26

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28

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36

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43

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49

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58

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59

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89

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102

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113

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141

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142

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143

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146

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147

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152

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162

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171

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172

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173

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174

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181
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182

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183

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184

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186

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187

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213

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238

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244

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247

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248